



6

1/249

FIGURE 1

CCAATGCCCGGTGCGGTGGTGCAGGGTCTCGGGCTAGTCATGGCGTCCCCGTCTCGGAGAC
TGCAGACTAAACCAGTCATTACTTGTTCAGAGCGTTCTGCTAATCTACACTTTATTTTC
TGGATCACTGGCGTTATCCTTCTTGCAGTTGGCATTGGGGCAAGGTGAGCCTGGAGAATTA
CTTTCTCTTTAAATGAGAAGGCCACCAATGTCCCCTCGTGCCTATTGCTACTGGTACCG
TCATTATTCTTTGGGCACCTTGGTTGCTACCTGCCAGCTCTGCATGGATGCTA
AAACTGTATGCAATGTTCTGACTCTCGTTTTGGTCGAAGTGGTCGCTGCCATCGTAGG
ATTGTTTCAGACATGAGATTAAGAACAGCTTAAGAATAATTATGAGAAGGCTTGAAAGC
AGTATAACTCTACAGGAGATTATAGAACGCATGCAGTAGACAAGATCCAAAATACGTTGCAT
TGGTGTGGTGTACCGATTATAGAGATTGGACAGATACTAATTACTCAGAAAAGGATT
TCCTAAGAGTTGCTGTAAACTTGAAGATTGACTCCACAGAGAGATGCAGACAAAGTAAACA
ATGAAGGTTGTTTATAAAGGTGATGACCATTATAGAGTCAGAAATGGGAGTCGTTGCAGGA
ATTCCTTGGAGTTGCTTGCTTCCAAC TGATTGGAAATCTTCTCGCCTACTGCCWCTCTCG
TGCCATAACAAATAACCAGTATGAGATAGTGTTAACCCAATGTATCTGTGGCCTATT CCT
CTACCTTAAGGACATTAGGGTCCCCCTGTGAATTAGAAAGTTGCTTGGCTGGAGAACTG
ACAACACTACTGATAGACCAAAAAACTACACCAGTAGGTTGATTCAATCAAGATGTAT
GTAGACCTAAACTACACCAATAGGCTGATTCAATCAAGATCCGTGCTCGCAGTGGCTGAT
TCAATCAAGATGTATGTTGCTATGTTCTAAGTCCACCTTCTATCCCATTGATGTTAGATCG
TTGAAACCCGTATCCCTCTGAAACACTGGAAGAGCTAGTAAATTGTAATGAAGT



2/249

FIGURE 2

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA19902
><subunit 1 of 1, 245 aa, 1 stop, 1 unknown
><MW: -1, pI: 8.36, NX(S/T): 1
MASPSRRLQTKPVITCFKSVLLIYTFIFWITGVILLAVGIWGKVSLENYFSLLNEKATNVPF
VLIATGTVIILLGTFGCFATCRASAWMLKLYAMFLTLVFLVELVAAIVGFVFRHEIKNSFKN
NYEKALKQYNSTGDYRSHAVDKIQNTLHCCGVTDYRDWTDTNYYSEKGFPKSCCKLEDCTPQ
RDADKVNNEGCFIKVMTIISEMGVVAGISFGVACFQLIGIFLAYCXSRAITNNQYEIV
```

Important features of the protein:

Signal peptide:

amino acids 1-42

Transmembrane domains:

amino acids 19-42, 61-83, 92-114, 209-230,

N-glycosylation site.

amino acids 134-138

Tyrosine kinase phosphorylation site.

amino acids 160-168, 160-169

N-myristoylation site.

amino acids 75-81, 78-84, 210-216, 214-220, 226-232

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 69-80, 211-222



3/249

FIGURE 3

CCCACCGCGTCCGGCGCCGTGGCCTCGCGTCCATCTTGCCGTTCTCTCGGACCTGTCACAAA
GGAGTCGCGCCGCCGCCGCCGCCCTCCCTCCGGTGGGCCCGGGAGGTAGAGAAAGTCAGT
GCCACAGCCCCGACCAGCGCTGCTCTGAGCCCTGGGCACGCCGAACGGGAGGGAGTCTGAGGGT
TGGGGACGTCTGTGAGGGAGGGAACAGCCGCTCGAGCCTGGGGCGGGCGGACCGGACTGGG
GCCGGGGTAGGCTCTGAAAGGGCCGGAGAGAGGTGGCCTGGTCAGAACCTGAGAAACAA
GCCGAGAGGTTTCCACCGAGGCCCGCCTGAGGGATCTGAAGAGGTTCTAGAAGAGGGT
GTTCCCTTTGGGGTCCTCACCAAGAGGTTCTGGGTGCCCCCTCTGAGGGAGGCT
GCGGCTAACAGGGCCAGAACTGCCATTGGATGCCAGAAATCCCCGTAGTTGATAATGTTG
GGAATAAGCTCTGCAACTTCTTGGCATTCAAGTTGTTAAAAACAAATAGGATGCAAATTCC
TCAACTCCAGGTTATGAAAACAGTACTTGGAAAAGTACCTAAATGATCGTCTTG
GTTGGGCCGTGTTCTTAGCGAGCAGAACGCCCTGGCCAGGGTCTGTTGACTCTCGAAGAG
CACATAGCCCACCTCCTAGGGACTGGAGGTGCCGCTACTACCATGGTAATTCTGTATCTG
CCGAGATGACAGTGGAACAGATGACAGTGTTGACACCCAACAGCAACAGGCCGAGAACAGTG
CAGTACCCACTGCTGACACAAGGAGCCAACCACGGGACCCCTGTCGGCCACCAAGGAGGGC
CGAGGACCTCATGAGCCAAGGAGAAAGAAACAAATGTGGATGGCTAGTGTGGACACACT
GGCAGTAATACGGACTCTGAGATAAGTAAGTATCTGACTCACGGTCACCTCCAGTGGAAAT
AAAAAGTGTCTGCCCGAACCATGACTTTAGGACTCCTCAGTCCTTAGGACATACTCG
CCAAGCCTTGTGCTCACAGGGCAAAGGAGAATATTTAATGCTCCGCTGATGGCAGAGTAAA
TGATAAGATTGATTTGCTTGCTGTCATCTACTTGTCTGGAAATGTCTAAATGTTCTG
TGTAGCAGAAAACACGATAAGCTATGATCTTATTAGAG



4/249

FIGURE 4

MIVFGWAVFLASRSLGQGLLLTLÉEHIAHFLGTGGAATTMGNSCICRDDSGTDDSVDTQQQQ
AENSAVPTADTRSQPRDPVRPPRRGRGPHEPRRKKQNDGLVLDTLAVIRTLVDKO

Signal peptide:

amino acids 1-16

Casein kinase II phosphorylation site.

amino acids 22-26, 50-54, 113-117

N-myristoylation site.

amino acids 18-24, 32-38, 34-40, 35-41, 51-57



5/249

FIGURE 5

GGCACGAGGCCTGTCCACCCGGGGCGTGGGAGTGAGGTACCAAGATTAGCCCATTGGCC
CCGACGCCTCTGTTCTCGGAATCCGGGTGCTCGGATTGAGGTCCC GGTTCTAACGGACTG
CAAGATGGAGGAAGGCAGGAACCTAGGAGGCCTGATTAAGATGGTCCATCTACTGGTCTTGT
CAGGTGCCTGGGCATGCAAATGTGGGTGACCTTCGTCAGGCTCCTGCTTTCCGAAGC
CTTCCCCGACATACTTCGGACTAGTGCAGAGCAAACCTTTCCCCTACTTCCACATCTC
CATGGGCTGTGCCTTCATCAACCTCTGCATCTGGCTTCACAGCATGCTTGGGCTCAGCTCA
CATTCTGGGAGGCCAGCCAGCTTACCTGCTGTTGAGCCTTACGCTGGCCACTGTCAAC
GCCCGCTGGCTGGAACCCCGCACCACAGCTGCCATGTGGGCCCTGCAAACCGTGGAGAAGGA
GCGAGGCCTGGGTGGGGAGGTACCAAGGCAGCCACCAGGGTCCGATCCCTACCGCCAGCTGC
GAGAGAAGGACCCCAAGTACAGTGCTCTCCGCCAGAATTCTCGCTACCATGGCTGTCC
TCTCTTGCAATCTGGCTGCGTCCTGAGCAATGGCTCTGCTCGCTGGCCTGCCCTGGA
AATAAGGAGCCTCTAGCATGGGCCCTGCATGCTAATAATGCTTCTTCAGAAATGAAAAAAA
AAAAAAAAAAAAA



6/249

FIGURE 6

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56107

<subunit 1 of 1, 231 aa, 1 stop

<NX(S/T): 0

MEEGGNLGGLIK MVHLLVLSGA WGMQM WVT FVSGFLLFRSL PRHT FGLVQSKL FPYFHISM
GCAFINLCILASQHAWAQLTFWEASQLYLLFLSLTLATVNARWLEPRTTAAMWALQTVEKER
GLGGEVPGSHQGPDPYRQLREKDPKYSALRQNFFRYHGLSSLCNLGCVLSNGLCLAGLALEIRSL

Signal peptide:

amino acids 1-24

Transmembrane domain:

amino acids 86-103, 60-75

Casein kinase II phosphorylation site.

amino acids 82-86

Tyrosine kinase phosphorylation site.

amino acids 144-151

N-myristoylation site.

amino acids 4-10, 5-11, 47-53, 170-176, 176-182

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 54-65

G-protein coupled receptors proteins.

amino acids 44-85



7/249

FIGURE 7

AATT CAG ATTT AAG CCC ATT CTG CAG TGG AATT CAT GAA CT AG CA AG AGG AC ACC AT CTT
CTT GT ATT ATA CA AGA AAG GAG TGT ACCT ATC ACAC ACAG GGGG AAAA **ATG** CT CTT TGG GT
GCT AGG CCT CCT AAT CCT CTG GG TTT CTG GG ACT CGT AA AGG AAAA CT AA AG ATT GA AG
AC AT CACT GATA AGT AC AT TTT ATC ACT GG AT GT GACT CGG CTT GG AA AC TT GG CAG CC
AG AACT TT GATA AAAA AGG GAT TT CAT GT AAT CG CT GC CT GT CT GACT GA AT CAGG AT CA AC
AG CT TT AA AGG CAG AA AC CT CAG AG AG ACT TC GT ACT GT GCT CT GG AT GT GACC GAC CC AG
AG AAT GT CA AG AGG ACT GCCC AGT GGG GT GA AG AACC AA AGT TT GGG GAG AA AGG TCT CT GGG GT
CT GAT CA AT AAT GCT GGT GT TCCC GG CGT GG CT CCC ACT GACT GG CT GAC ACT AGAG GA
CT AC AG AGA AC CT ATT GA AGT GA AC CT GT TT GG ACT CAT CAGT GT GAC ACT AA AT AT GCT TC
CTT GGT CA AG AA AG CT CA AGG GAG GT ATT AAT GT CT CC AGT GT GG AG GT CG CTT GCA
AT CG TT GG AG GGG GCT AT ACT CC AT CCA AA AT AT GCA GT GG AA AG GT TT CA AT GAC AG CT TA AG
AC GGG AC AT GAA AG CT TT GGT GT GC AC GT CT CAT GC ATT GA ACC AGG GAT GT CA AA AC AA
ACT TGG CAG AT CC AGT AA AG GT ATT GA AAAA AA ACT CG CC AT TT GGG GAG CAG CT GT CT CC A
GA CAT CAA ACA ACA AT AT GG AGA AG GT TAC ATT GA AAAA AGT CT AG AC AA ACT GAA AGG CAA
TAA AT CCT AT GT GA AC AT GG AC CT CT CC GG GT GG TAG AGT GC AT GG ACC AC GCT CT AA CAA
GT CT CT CC CT AAG ACT CATT AT GCG CT GG AAAA AG AT GC CAA AA ATT TT CT GG AT AC CT TG
TCT CAC AT GCC AG CAG CT TG CA AG ACT TT TATT GT GA AA AC AG AA AG CAG AG CT GG CT AA
TCC CA AGG CAG T **TGA** CT CAG CT AAC CAA AT GT CT CC CAG GCT AT GAA AT TG GCC GAT
TT CA AG A AC AC AT CCT CT TT CA ACC CC ATT CCT AT CT GCT CC AAC CT GG ACT CATT AGA
TC GT GCT ATT GG ATT GCA AA AGG GAG TCC ACC AT CG CT GG GT AT CC CAG GGT CC CT G
CT CA AG TT TCTT GAA AA AGG AGG GCT GG AAT GGT AC AT CAC AT AGG CA AG T C CT G C C T GT
ATT TAGG CTT GC CT GCT GG GT GAT GT AAGG AA ATT GAA AG ACT T G C C ATT CAA AT G
AT CTT ACC GT GG C CT G C C C AT GCT AT GG T C C C AG C ATT AC AG T A ACT GT GA AT GT T
AAG T AT C AT CT CT AT CTA AA AT ATT AAA AG AT AAG T CA ACC C AAAA AAAAAA AAAAAA
AAAAA AAAAAA AAAAAA AAAAAA



8/249

FIGURE 8

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56406
><subunit 1 of 1, 319 aa, 1 stop
><MW: 35227, pI: 8.97, NX(S/T): 3
MLFWVLGLLILCGFLWTRKGKLKIEDITDKYIFITGCDSGFGNLAARTFDKKGFHVIAACLT
ESGSTALKAETSERLRTVLLDVTDPENVKRTAQWVKNQVGEKGLWGLINNAGVPGVLAPTDW
LTLEDYREPIEVNLFGlisVTLNMLPLVKKAQGRVINSSVGGRLAIVGGGYTPSKYAVEGF
NDSSLRRDMKAFGVHVSCIEPGLFKTNLADPVKVIEKKLAIWEQLSPDIKQQYGEFYIEKSLD
KLKGNKSYVNMDLSPVVECMDHALTSLFPKTHYAAGKDAKIFWIPLSHMPAALQDFLLLKQK
AELANPKAV
```

Important features of the protein:

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 136-152

N-glycosylation sites.

amino acids 161-163, 187-190 and 253-256

Glycosaminoglycan attachment site.

amino acids 39-42

N-myristoylation sites.

amino acids 36-41, 42-47, 108-113, 166-171, 198-203 and 207-212



9/249

FIGURE 9

GCGGGCTGTTGACGGCGTGC~~G~~**A**TGGCTGCCTGCGAGGGCAGGAGAACGGAGCTCTCGGTT
CCTCTCAGTCGGACTCCTGACGCCAGTGGCGGGGCCCTGGGCCGTGCCACCCT
GTAGTCATGTACCCACCGCCGCCGCCCTCATCGGGACTTCATCTCGGTGACGCTGAG
CTTGCGAGAGCTATGACAACAGCAAGAGTTGGCGCGCTCGTGGAGGAATGGA
AGCAACTGTCGAGATTGACGCGGAATATGATTCTCTCCTGCCTTCTGCTTTCTGT
GGACTCCTCTTACATCAACTGGCTGACCATGGAAAGCTCTGGCTTCAGGCTAGAGGA
AGAGCAGAAGATGAGGCCAGAAATTGCTGGTTAAAACCAGCAAATCCACCCGCTTACACAG
CTCCTCAGAAGGCCACCCGACACTGAGACTTACCTGAGATTTCGTACAGAAGACACAA
AGACACATCCAGCGGGGACACCTCACCTGCAGATTAGACCCCCAAGCCAAGACCTGAAGGA
TGGGACCCAGGAGGAGGCCACAAAAAGGCAAGAACGCCCCTGTGGATCCCCGCCGAAGGAG
ATCCGCAGAGGACAGTCAGCTGGAGGGAGCGGTGATCGAGCCTGAGCAGGGCACCGAG
CTCCCTCAAGAAGAGCAGAAGTGCCCACCAAGCCTCCCTGCCACCGGCCAGGACACAGGG
CACACCAGTGCATCTGAACATCGCCAGAAGGGCGTGTGGATTCAGTCTGCATGCATGG
AAGGATACCGCAAGTTGCATGGGCCATGACGAGCTGAAGCCTGTGTCCAGGCTTCAGT
GAGTGGTTGGCCTGGTCTCACACTGATCGACGCGCTGGACACCATGTGGATCTGGTCT
GAGGAAGAATTGAGGAAGCCAGGAAGTGCGAAGAAGTTACACTTGAAGGACG
TGGACGTCAACCTGTTGAGAGCACGATCCGATCCTGGGGGCTCTGAGTGCCTACAC
CTGTCGGGACAGCCTCTGGAGGAAAGCTGAGGATTTGGAATCGGCTAATGCCTGC
CTTCAGAACACCATCCAAGATTCTACTCGGATGTGAACATCGGTACTGGAGTTGCCACC
CGCCACGGTGGACCTCCGACAGCACTGTGGCGAGGTGACCAGCATTAGCTGGAGTTCCGG
GAGCTCTCCGTCTCACAGGGATAAGAAGTTCAAGGAGGAGTGGAGAACGGTACAGCA
CATCCACGGCCTGCTGGGAAGAAGGATGGCTGGTGCCTGTTCAATACCCACAGTG
GCCTCTTCACCCACCTGGCGTATTCACTGCTGGCGCCAGGGCGACAGCTACTATGAGTAC
CTGCTGAAGCAGTGGATCCAGGGCGGAAGCAGGAGACACAGCTGCTGGAGACTACGTGGA
AGCCATCGAGGGTGTCAAGAACGACCTGCTGGCAGTCCGAGCCCAGTAAGCTCACCTTG
TGGGGAGCTTGCCTGGCGCTTCAGTGCCAAGATGGACCACCTGGTGTGCTTCTGCCA
GGGACGCTGGCTCTGGCGTCTACCACGGCCTGCCGCCAGCCACATGGAGCTGGCCCAGGA
GCTCATGGAGACTGTTACAGATGAACCGCAGATGGAGACGGGCTGAGTCCCAGATCG
TGCACCTCAACCTTACCCCCAGCCGGCGTCGGACGTGGAGGTCAAGCCAGCAGACAGG
CACAACCTGCTGCGGCCAGAGACCGTGGAGAGCCTGTTCTACCTGACCGCTCACAGGGGA
CCGCAAATACCAGGACTGGGCTGGAGATTCTGAGGCTTCAGCCGATTACACGGGTCC
CCTCGGGTGGCTATTCTCCATCAACAATGTCAGGATCCTCAGAACGGCGAGCCTAGGGAC
AAGATGGAGAGCTTCTCCTGGGGAGACGCTCAAGTATCTGTTCTGCTCTCCGATGA
CCAAACCTGCTCAGCCTGGACGCCCTACGTGTTCAACACCGAACGCCACCCCTGCCTATCT
GGACCCCTGCC**TAG**GGTGGATGGCTGCTGGTGTGGGACTTCGGGTGGCAGAGGCACCTG
CTGGGTCTGTCATTTCAAGGGCCACGTAGCACCGCAACCGCCAAGTGGCCAGGGCT
CTGAACTGGCTCTGGCTCCTCGTCTGCTTAAATCAGGACACCGTGAGGACAAGTGA
GCCGTCAGTCTGGTGTGATGCGGGGTGGGCTGGAGCCTCCGCTGCTTCTC
CAGAACACGAATCATGACTCACGATTGCTGAAGCCTGAGCAGGTCTGTGGGCCAGGA
GAGGGGGCTCGAGGTGGTCCCTGGTACTGGGGTGACCGAGTGGACAGCCCAGGGTGAGC
TCTGCCGGCTCGTGAAGCCTCAGATGTCCCCAATCCAAGGGCTGGAGGGCTGCCGTGA
CTCCAGAGGCCTGAGGCTCCAGGGCTGGCTGGTGTGTTACAAGCTGGACTCAGGGATCCTC
CTGGCCGCCCGCAGGGGCTTGGAGGGCTGGACGGCAAGTCCGTCTAGCTCACGGCCCT
CCAGTGGAAATGGGTCTTTCGGTGGAGATAAAAGTTGATTTGCTCTAACCGCAA



10/249

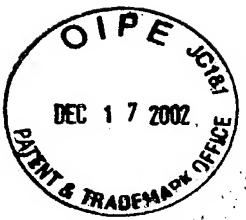
FIGURE 10

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56529
><subunit 1 of 1, 699 aa, 1 stop
><MW: 79553, pI: 7.83, NX(S/T): 0
MAACEGRRSGALGSSQSDFLT PPGVGGAPWA VATTVV MYP PPPPPP HRDF ISVTLSFGESYDN
SKSWRRRSCWRKWKQLSRLQRNMILFLLAFL FCGLLFYINLADHWKALAFRLEEEQKMRPE
IAGLK PANPPVLPAPQKADTD PENLPEISSQKTQRHIQRGP PHLQIRPPSQDLKDGTQEEAT
KRQEAPVDP RPEGDPQRTVISWRGA VIEPEQGT ELP SRAEVPTK PPLP PARTQGT PVHL NY
RQKG VIDVFLHAWKGYRKFAWGHDELKPVSRSFSEWFG LGLTLIDALDTM WILGLRKEFEEA
RKWVSKKLHFEKDV DVL FESTIRI LGGLL SAYHLSGDSLFLRKAEDFGNRLMPA FRTP SKI
PYSDVNIGTGVAHPPRWTSDSTVAEVT SIQLEFRELSRLTGDKKF QEA VEKVTQH IGLSGK
KDGLVPMFIN THSGLFT HLG VFTL GARAD SYYE YLLK QWIQGGKQET QLLED YVEAIEGV RT
HLLRHSEPSKLT FVGELAHGRFSAKMDHLVCFLPGTLALGVYHGLPASHMELAQELMETCYQ
MNRQMETGLSPEIVHF NLYPQPGR RDVEVKPADRHNLLRPETVESLFYLYRVTGDRKYQDWG
WEILQSFSRFTRVPSGGYSSINNVQDPQKPEPRDKMESFFLGETLKYLFL FSDDPNLLSLD
AYVFNTEAHPLPIWTPA
```

Important features of the protein:

Transmembrane domain:

amino acids 21-40 and 84-105 (type II)



11/249

FIGURE 11

GGCGCCGCGTAGGCCCGGGAGGCCGGCCGGCCGGCTGCGAGCGCCTGCCCATGCGCCGC
CGCCTCTCCGCACGATGTCCCCCTCGCGAGGAAAGCGCGCAGCTGCCCTGGGAGGACGGC
AGGTCCGGTTGCTCTCCGGCGGCCTCCCTCGGAAGTGTTCGTCTTCCACCTGTTGTGGC
CTGCCTCTCGCTGGCTTCTTCTCCCTACTCTGGCTGCAGCTCAGCTGCTCTGGGGACGTGG
CCCGGGCAGTCAGGGACAAGGGCAGGAGACCTCGGGCCCTCCCCTGCCTGCCCTGGCAGTGGT
CCGCCCCCTGAGCACTGGGAAGAAGACGCATCCTGGGGCCCCACCGCCTGGCAGTGTGGT
GCCCTCCCGGAACGCTTCGAGGAGCTCTGGTCTCGTGCCACATGCGCCGCTTCCTGA
GCAGGAAGAAGATCCGGCACCATCTACGTGCTAACCAAGGTGGACCACCTCAGGTTAAC
CGGGCAGCGCTCATCAACGTGGCTTCCTGGAGAGCAGAACAGCACGGACTACATTGCCAT
GCACGACGTTGACCTGCTCCCTCAACGAGGAGCTGGACTATGGCTTCCTGAGGCTGGC
CCTTCCACGTGGCCTCCCCGGAGCTCCACCCCTCTACCACTACAAGACCTATGCGCCGG
ATCCTGCTGCTCTCCAAGCAGCACTACCGGCTGTGCAATGGGATGTCCAACCGCTCTGGGG
CTGGGGCCCGAGGGACGACGGAGTTCTACCGGCGATTAAGGGAGCTGGCTCCAGCTTTCC
GCCCTCGGAATCACAACGGTACAAGACATTGCCACCTGCATGACCCAGCCTGGCG
AAGAGGGACCAGAAGCGATCGCAGCTCAAAAACAGGGAGCAGTTCAAGGTGGACAGGGAGGG
AGGCCTGAACACTGTGAAGTACCATGTGGCTCCCGACTGCCCTGTCTGTGGCGGGGCC
CCTGCACTGTCTCAACATCATGTTGGACTGTGACAAGACCGCCACACCCCTGGTGCACATT
AGCTGAGCTGGATGGACAGTGAGGAAGCCTGTACCTACAGGCCATATTGCTCAGGCTCAGGA
CAAGGCCTCAGGTGTTGGCCAGCTCTGACAGGATGTGGAGTGGCCAGGACCAAGACAGCA
AGCTACGCAATTGCAGCCACCCGGCCAGCTCAAGGCAGGCTGGCTGGCCAGGACACGTGGG
GTGCCTGGACGCTGCTTGCATGCACAGTGATCAGAGAGAGGCTGGGTGTGCCTGTCCG
GGACCCCCCTGCCTTCTGCTCACCCCTACTCTGACCTCCTCACGTGCCAGGCCTGTGGG
TAGTGGGGAGGGCTGAACAGGACAACCTCTCATCACCCACTCTGACCTCCTCACGTGCC
AGGCCTGTGGTAGTGGGAGGGCTGAACAGGACAACCTCTCATCACCCCCAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAA



12/249

FIGURE 12

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56531
><subunit 1 of 1, 327 aa, 1 stop
><MW: 37406, pI: 9.30, NX(S/T): 1
MFPSSRRKAAQLPWEGRSGLLSGGLPRKCSVFHLFVACLSLGFFSLLWLQLSCSGDVARAVR
GQGQETSGPPRACPPEPPPEHWEEDASWGPHRLAVLVPFRERFEELLVFVPHMRRFLSRKKI
RHHIYVLNQVDHFRFNRAALINVGFLESSNSTDYIAMHDVDLLPLNEELDYGFPEAGPFHVA
SPELHPLYHYKTYVGGILLSKQHYRLCNGMSNRFWGWRGREDDEFYRIKAGLQLFRPSGI
TTGYKTFRHLHDPAWRKRDQKRIAQQKQEKFVDRREGGLNTVKYHVVASRTALSVGGAPCTVL
NIMLDCKTATPWCTFS
```

Signal peptide:

amino acids 1-42

Transmembrane domain:

amino acids 29-49 (type II)

N-glycosylation site.

amino acids 154-158

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 27-31

Tyrosine kinase phosphorylation site.

amino acids 226-233

N-myristoylation site.

amino acids 19-25, 65-71, 247-253, 285-291, 303-309, 304-310



13/249

FIGURE 13

CAATGTTGCCTATCCACCTCCCCAAGCCCCCTTACCTATGCTGCTGCTAACGCTGCTGCT
GCTGCTGCTGCTGCTAAAGGCTCATGCTGGAGTGGGACTGGTCGGTGCCAGAAAGTCT
CTTCTGCCACTGACGCCCATCAGGGATTGGGCCTCTTCCCCCTCCTTGTGTCTC
CTGCCTCATGGCCTGCCATGACCTGCAGCCAAGCCCAGCCCCGTGGGAAGGGGAGAAAGT
GGGGGATGGCTAAAAAGCTGGAGATAGGAACAGAACAGGGTAGTGGGTGGGCTAGGGGG
GCTGCCTATTAAAGTGGTTGTTATGATTCTTATACTAATTATAACAAAGATATTAAGGC
CCTGTTCATTAAGAAATTGTTCCCTCCCTGTGTTCAATGTTGTAAAGATTGTTCTGTGT
AAATATGTCTTATAATAACAGTTAAAGCTGAAAAAAA



SEARCHED SERIALIZED INDEXED

14/249

FIGURE 14

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56862
<subunit 1 of 1, 73 aa, 1 stop
<MW: 7879, pI: 7.21, NX(S/T): 0
MLLLTLLLLLKGSCLEWGLVGAQKVSSATDAPIRDWAFFPPSFLCLLPHRPAMTC
SQAQ
PRGEGEKVGDG
```

Important features:

Signal peptide:

amino acids 1-15

Growth factor and cytokines receptors family:

amino acids 3-18



FIGURE 15

GGGACCCATGCAGGCCGTGACCCCCGGCTCCCTAGAGGCCAGCGCAGCCGAGCGGACAAAG
GAGCATGTCCCGCGCCGGGGAGGGCCGTCCTCCGGCCATAAGGCTCCGGTCGCCGCTGG
GCCCGCGCCGCGCTCCTGCCGCCGGCTCCGGGGCGCCGCTAGGCCAGTGCAGCCGCCG
CTCGCCCCCGCAGGCCCGGCCGAGCAGC**ATG**GAGGCCACCCGGACGCCGGGGCCGCGCA
GCCGCCGCTGTTGCTGCCGCTCGCTGTTAGCGCTGCTCGCCTGCTGGGAGGCAGGCCG
GCGGCCGCGCCGCCGCGCTGCCGCCGGCTGCAAGCACGATGGCGGCCGGAGGGGCTGG
AGGGCGGCCGGCGCCGAGGGCAAGGTGGTGTGCAGCAGCCTGGAACTCGCCAGGTCT
GCCCGCAGATACTCTGCCAACCGCACGGTACCCCTGATTCTGAGTAACAATAAGATATCCG
AGCTGAAGAATGGCTCATTTCTGGGTTAAGTCTCCTGAAAGATTGGACCTCGAAACAAT
CTTATTAGTAGTATAGATCCAGGTGCCTCTGGGACTGTCATCTCTAAAAAGATTGGATCT
GACAAACAATCGAATAGGATGTCTGAATGCAGACATATTCGAGGACTCACCAATCTGGTC
GGCTAAACCTTCGGGAATTGTTCTTCATTATCTCAAGGAACCTTGATTATCTTGC
TCATTACGGTCTTGGATTCCAGACTGAGTATCTTGTGTGACTGTAACATACTGTGGAT
GCATCGCTGGTAAAGGAGAAGAACATCACGGTACGGGATACCAGGTGTGTTATCCTAAGT
CACTGCAGGCCAACCGACTCACAGCGTGAAGCAGGAGCTGTCAGATGCGACCCCTCCGCT
GAATTGCCGTCTTCTACATGACTCCATCTCATGCCAAGTTGTGTTGAAGGAGACAGCCT
TCCTTCCAGTGCATGGCTCATATATTGATCAGGACATGCAAGTGTGTTGAGGATG
GGAGAATAGTTGAAACCGATGAATCGCAAGGTATTTGTTGAAAAGAACATGATTCAAAC
TGCTCCTGATTGCAAGTGCCCTAACCATTTCTAATATTCAAGGCTGGATCTACTGGAAATTG
GGGCTGTATGTCCAGACCAACGTGGGAATAATACGAGGACTGTGGATATTGGTATTAG
AGAGTTCTGCACAGTACTGCTCCAGAGAGGGTGTAAACAACAAAGGTGACTTCAGATGG
CCCAGAACATTGGCAGGCATTACTGCATATCTGCAGTGTACGGGAACACCCATGGCAGTGG
GATATATCCGGAAACCCACAGGATGAGAGAAAAGCTGGCGAGATGTGATAGAGGTGGCT
TTGGCAGATGATGATTATTCTCGCTGTCACTGCAAATGATGTCACTAGAGTTCTTAT
ATGTTAACATCAGATGCCCTCAATCTTACCAATGCCGTGGCAACAGCTGACAGTTACTGG
TTACACTGTGGAAGCAGCCAACCTTCTGACAAAATGGATGTTATATTGTGGCAGAAATGA
TTGAAAATTGGAAAGATTACCAAGGAGAAAATCAAAGAGCTAGGTGACGTGATGGTT
GACATTGCAAGTAACATCATGTTGGCTGATGAACGTGCTGTGGCTGGCAGAGGGAAAGC
TAAAGCCTGCAGTAGGATTGTGCAGTGTCTCAGCGCATTGCTACCTACCGCTAGCCGGTG
GAGCTCACGTTATTCAACATATTACCCAAATTGCTCTGGAAAGCTTATGTCATCAAGTCT
ACTGGCTTCACGGGATGACCTGTACCGTGTCCAGAAAGTGGCAGCCTCTGATCGTACAGG
ACTTTCGGATTATGGAGGGGGATCCAGAGGGAAACCTGGATAAGCAGCTGAGCTTAAAGT
GCAATGTTCAAATACATTTCGAGTCTGGCACTAAAGGTATGTTACATTCTGCAATCATT
AAGACTATTACAGT**TAA**ATTAGAATGCTCAAATGTTCTGCTTCAGGTTAAAGAAA
AAAGATTTTTTGCAGGAAGATAGGTATTATTGCTTTGCTACTGTTAAAGAAA
ACCAGGAAGAACTGCATTACGACTTCAAGGGCCCTAGGCATTGCTTGTGCTTAAAG
CTTCACATAAAATATCAGAAATTACATTATACTGCAAGTGGTATAAAATGCAAATATACT
ATTGTTACATGTGAAAAAATTATTGACTTAAAGTTATTATTGTTTTGCTCCT
GATTTAACACAATAAGATGTTCTGGCCCTAAAGTATCATGAGCCTTGGCACTGC
GCCTGCCAAGCCTAGTGGAGAAGTCACCCCTGAGACCAGGTGTTAACTCAAGCAAGCTGTAT
ATCAAAATTGGCAGAAAACACAAATATGTCATATCTTTTAAAGTATTCA
TTGAAGCAAGCAAATGAAAGCATTGTTACTGATTTAAAGTTGGTCTTAGATATATT
GACTACACTGTATTGAAGCAAATAGAGGAGGCACAACCTCCAGCACCCATAATGGAACCACATT
TTTTCACTTAGCTTCTGTGGCATGTGTAATTGTATTCTGCGGTTTTAATCTCACAG
TACTTATTCTGTCTGTCCTCAATAATCACAAACAATATTCCAGTCATTAAATGGC
TGCATAATAACTGATCCAACAGGTGTTAGGTGTTAGTGTGAGCACTCAATAAATA
TTGAATGAATGAACGAAAAAAAAAAAAAA



16/249

FIGURE 16

MEPPGRRRGRAQPPLLPLSLLALLALLGGGGGGAAALPAGCKHDGRPRGAGRAAGAAEGK
VVCSSLELAQVLPPDTLPNRTVTLLISNNKISELKNGSFSGLSLLERLDLRNNLISSIDPGA
FWGLSSLKRDLTNRIGCLNADIFRGLTNLVRNLSGNLFSSLSQGTFDYLASLRSLEFQT
EYLLCDCNILWMHRWVKEKNITVRDTRCVYPKSLQAQPVTGVKQELLCDPPELPSFYMTP
SHRQVVFEGDSLFPQCMASYIDQDMQVLWYQDGRIVETDESGQIFVEKNMIHNCSLIASALT
ISNIQAGSTGNWGCHVQTKRGNNRTVDIVVLESSAQYCPPERVVNNKGDFRWPRTLAGITA
YLQCTRNTHGSGIYPGNPQDERKAWRRCDRGGFWADDYSRCQYANDVTRVLYMFNQMPLNL
TNAVATARQLLAYTVEAANFSDKMDVIFVAEMIEKFGRFTKEEKSKELGDVMVDIASNIMLA
DERVLWLAQREAKACSRIVQCLQRIATYRLAGGAHVYSTYSPNIALEAYVIKSTGFTGMTCT
VFQKVAASDRTGLSDYGRRDPEGNLDKQLSFKCNVSNTFSSLALKVCYILQSFKTIYS

Signal peptide:

amino acids 1-33

Transmembrane domain:

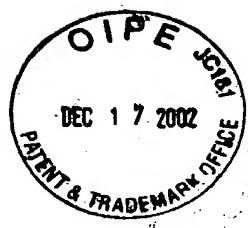
amino acids 13-40 (type II)

N-glycosylation site.

amino acids 81-85, 98-102, 159-163, 206-210, 301-305, 332-336,
433-437, 453-457, 592-596

N-myristoylation site.

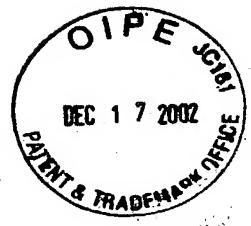
amino acids 29-35, 30-36, 31-37, 32-38, 33-39, 34-40, 51-57,
57-63, 99-105, 123-129, 142-148, 162-168, 317-323, 320-326,
384-390, 403-409, 554-560



17/249

FIGURE 17

GCGTGGGGATGTCTAGGAGCTCGAAGGTGGT GCTGGGCCTCTCGGTGCTGCTGACGGCGGCC
ACAGTGGCCGGCGTACATGTGAAGCAGCAGTGGACCAGCAGAGGCTTCGTGACGGAGTTAT
CAGAGACATTGAGAGGCAAATTGGAAAAAGAAAACATTGCTTTGGAGAACAGATTAA
TTTGACTGAGCAACTGAAAGCAGAAAGAGAGAAGATGTTATTGGCAAAAGGATCTAAAAA
TCATGACTTGAATGTGAAATATCTGTTGGACAGACAACACAGAGTTGTGTGTGTTGAT
GGAGAGTAGCTTAGTGTACTCTTCATCTTTGGTCAGTCCTTTAAACTTGATCA
AATAAAGGACAGTGGGTCAATAAGTTACTGCTTCAGGGCCCTTATATCTGAATAAAGGA
GTGTGGGCAGACACTTTGGAAGAGTCTGTCTGGGTGATCCTGGTAGAAGCCCCATTAGGG
TCACTGTCCAGTGCTTAGGGTTGTTACTGAGAAGCACTGCCAGCTGTGAGAAGGAAGGGA
TGGATAGTAGCATCCACCTGAGTAGTGTGATCAGTCGGCATGATGACGAAGCCACGAGAACAA
TCGACCTCAGAAGGACTGGAGGAAGGTGAAGTGGAGGGAGAGACGCTCCTGATCGTCGAATCC



18/249

FIGURE 18

MSRSSKVVLGLSVLTAATVAGVHVKQQWDQQRLRDGVIRDIERQIRKKENIRLLGEQIILT
EQLEAEREKMLLAKGQSQKS

Signal peptide:

amino acids 1-21



19/249

FIGURE 19

CTGTCGTCTTGGCTTCAGCCGCAGTCGCCACTGGCTGCCTGAGGTGCTCTACAGCCTGTT
CAAAGTGTGGCTTAATCCGTCTCCACCACCAAGATCTTCTCCGTGGATTCCCTTGCTAAGACC
GCTGCCATGCCAGTGACGGTAACCCGCACCACCATCACAAACCACGACGTACATCTCGGG
CCTGGGGTCCCCCATGATCGTGGGGTCCCCTGGGCCCTGACACAGCCCTGGGTCTCCTTCGC
CTGCTGCAGCTGGTGTCTACCTGCCTGGCCTTCGCTGGTGGCTAGCGTGGCGCTGGAC
GGGGTCCATGGGCAACTGGTCCATGTTCACCTGGTGCTTCTGCTTCTCCGTGACCGTGATCA
TCCTCATCGTGGAGCTGTGCAGGCTCCAGGCCGCTCCCCCTGCTTGGCGCAACTCCCC
ATCACCTCGCCTGCTATGCAGGCCCTCTGCCTCTGCCCTCCATCATCACCCCCACAC
CTATGTCCAGTTCTGTCCCACGGCGTTCGCGGGACCACGCCATGCCGCCACCTCTTCT
CCTGCATCGCGTGTGGCTTACGCCACCGGAAGTGGCTGGACCCGGGCCGGCGAG
ATCACTGGCTATATGCCACCGTACCCGGGCTGCTGAAGGTGCTGGAGACCTCGTTGCCTG
CATCATCTCGCGTTCATCAGCACCCAACCTGTACCGACCCAGCCGGCCCTGGAGTGGT
GGCGTGGCGGTGTACGCCATCTGCTTCATCCTAGCGGCCATGCCATCCTGCTGAACCTGGGG
GAGTGCACCAACGTGCTACCCATCCCCCTCCCCAGCTCCTGTCGGGGCTGGCCTGCTGTC
TGTCCCTCTATGCCACGCCCTGTTCTGGCCCTCTACAGTTGATGAGAAGTATG
GCCGCCAGCCTCGCGCTCGAGAGATGTAAGCTGCAGCCGAGCCATGCCACTACGTGTG
GCCTGGGACCGCCACTGGCTGTGGCCATCCTGACGCCATCACCTACTGGCGTATGTGGC
TGACCTGGTGCACTCTGCCACCTGGTTTTGTCAAGGTCTAAACTCTCCAAGAGGCTCC
CGTCCCTCTCCAACCTCTTGTCTTCTGCCAGGTTCTTATGGAGTACTTCTTCC
TCCGCCTTCCTCTGTTCTTCTTCTGCCCTCCACCTTTCTTCCT
CAATTCCCTGCACTCTAACAGTTCTGGATGCATCTTCTGCCCTTCTGCTGT
TTCTTCTGTGTTGTTGCCACATCCTGTTCTTCAACCTGAGCTGTTCTCTTT
CTTTCTTCTTTTTTTTTTAAGACGGATTCTCACTCTGTGGCCAGGCTGGAG
TGCAGTGGTGCATCTCAGCTCACTGCAACCCCCGCCTCCTGGGTTCAAGCGATTCTCTCC
CCCAGCCTCCAAAGTAGCTGGGAGGACAGGTGTGAGCTGCCGCACCCAGCCTGTTCTCTT
TTCCACTCTCTTCTCATCTCTTCTGGGTTGCCCTGTCGGCTTATCTGCCTGT
TTGCAAGCACCTCTCCTGTGTCCTGGAGCCCTGAGACTTCTTCTCCTGCCCTCCA
CCCACCTCAAAGGTGCTGAGCTCACATCCACACCCCTGCAGCCGTCATGCCACAGCCCC
CCAAGGGGCCATTGCCAAAGCATGCCCTGCCACCCCTCGCTGTGCCTTAGTCAGTGTGAC
GTGTGTGTGTGTGTTGGGGGTGGGGGTGGTAGCTGGGATTGGCCCTCTTCT
CCCAGTGGAGGAAGGTGTGAGCTGACTTCCCTTAAATTAAAAACATATATATATAT
ATTTGGAGGTCAAGTAATTCCAATGGCGGGAGGCATTAAGCACCGACCCCTGGGTCCCTAGG
CCCCGCCTGGCACTCAGCCTGCCAGAGATTGGCTCCAGAATTGCCCCAGGCTTACAGAACAC
CCACTGCCTAGAGGCCATCTAAAGGAAGCAGGGCTGGATGCCTTACAGAACAC
CTGTGGTATGAAAAAG



20/249

FIGURE 20

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58727
<subunit 1 of 1, 322 aa, 1 stop
<MW: 35274, pI: 8.57, NX(S/T): 1
MPVTVRTTITTTTSSSGLGSPMIVGSPRALTQPLGLRLLQLVSTCVAFSLVASVGAWTG
SMGNWSMFTWCFCFSVTLIILIVELCGLQARFPLSWRNFPITFACYAALFCLSASIYPTTY
VQFLSHGRSRDHAIATFFSCIACVAYATEVAWTRARPGEITGYMATVPGLLKVLETFVACI
IFAFISDPNLYQHOPALEWCVAVYAIKFILAAIAILLNLGECTNVLPPIPFPSSLGALLSV
LLYATALVLWPLYQFDEKYGGQPRRSRDVSCSRSHAYYVCAWDRRLAVAILTAINLLAYVAD
LVHSAHLVFKV
```

Important features:

Transmembrane domains:

amino acids 41-60 (type II), 66-85, 101-120, 137-153, 171-192,
205-226, 235-255 and 294-312

N-glycosylation site.

amino acids 66-69

Glycosaminoglycan attachment site.

amino acids 18-21



21/249

FIGURE 21

GAACGTGCCACCATGCCCAAGCTAATTTGTATTTAGTAGAGACGGGGTTACCATGTTGGCCAGGCTGGTC
TTGAACTCGTGACCTCATGATCCGCTCACCTCGGCCTCCCAAAGTGTGGATTACAGGCATGAGCCACTGACGC
CTGGCCAGCCTATGCATTTAAAGAAATTATTCTGTATTAGGTGTGCTAACATGGCACTACAGTGACCA
AAACAGACTGAATTCCCCAAGAGCAAAGACCAAGTGAAGGGAGACCAACAAGAAACAGAAATGCAAAAGAGACCA
TTATTACTCACTATGACTAAGGGTCACAAATGGGTACGTGATGGAGAGTGATTTGTAAGAGACTACAGAGGG
AGGACAGACTACCAAGAGGGGGCAGGAAAGCTCCTCTGACGAGGTGGTATTCAGCCAAACTGGAAGAATGA
GAAAGAGCTAGCCAGCCATCAGAATAGTCCAGAAGAGATGGGGAGCACTACACTCACTACACTTGGCCTGAGAA
AATAGCATGGATTGGAGGAGGCTGGGGAACACCACCTCTGCCGACCTGGCAGGAGGCATTGAGGGCTTGAGA
AAGGGCAATGGCAGTAGCAGTAGAAAGGACAGGGTAGGGAGCAGGGACTTTGCAAGGTGGAATCATTAGGTCTTATC
AACAGATATGGGCAAGCAAAGCCAGGGGAGAATTGATGGTAATGCTGAGGTTGGAGCCAGGCTAGATGGGACAG
TGGTGGGTGATGCAAAGGAAAGAGGTCAAGGAAGCAGCAGGGCCAGACGTGGGGAGAAGGTGTGGGGTTGGTTCCA
TCTTGGCAGTCTGCCGAATGTGGATGGGAAGACCAAGAGGAGGAGCAAGGGGAGAGGGGAAGGGAATCTAA
AGAAGTCTGGATGCCACACTCTCTCCCTCTCCCTCTCCCTCTCCCTCAGAGGTCTCACTGTGGTTCTCAT
TTCCTGCCCTGCCCATCTCCCTGGGGTCTGGGAAGAAGTGGAGGATTAGCTGAAGGTTTGCTCTCGGGGCTG
TCTGAATCTCCATTGCTTCTGGGAGGACATAATTCACTCTGCTTAGCTTCTTATCATCTTACATTCCCTGTAG
CCACTGGGACATATGTGGTGTCTAGCTCTGCTAGCTCTGCTCATGCCCTTGCTGGGTATGGCATGTAG
GGGGAGGGTCAATTGCTGTCAAGAGGGCACTGACTTTCAATGGTGTACCAAGGTGAATGTTGGAGACACAGTC
GCGATGCTGCCCAAGTCCCAGGCAACTATCCAGGAGATCGCTGCCCTGGCAGGTCTCCCTGCATGGT
ATGCAGCCCCCTCCC**ATG**TTCTGGCCACTTTGTCCTTCTCCCTGCTAGGTGAATCTCAGCCCCCTCTCCACCCAAAGGTT
GTGAGTACATGCTGGGTCTCCCCTTCTCCCTGCTAGGTGAATCTCAGCCCCCTCTCCACCCAAAGGTT
ACATGGATCCTAACTACTGCCACCCCTCCACCTCCCTGCACCTGTGCTCCCTGGCCTGGTCCTTACAGGCTTC
TCCACCCCTCCCTATCTCAGGTATTCAGGTGGTAAGGACACGTGACCAAGCCTACGCCATGGCCAGG
GCCGAGTGGCTCACCTCATTGAGTGGAAAGGCTGGAGCAAGCCAGTGACTIONCCTGTCACCTGTCGCCCTGGAAATCAGCCT
TTCCCTCCTATTGACACCTCAGCGAGGGCAACAAGAGGCTCGCTTGAGCAGGAGTGGCTGAGCAGTTGCA
TCGCGGAAGCCAAGCTCGAGCATGGTCTCGGTGGATGGCGAGGACTCCACTGATGACTCCTATGATGAGGACT
TTGCTGGGGAAATGGACACAGACATGGCTGGCAGCTGCCCTGGGGCCACCTCCAGGACCTGTCACCGGCC
ACCGGTTCTCCGGCCCTGCGCAGGGCTCCCGTGGAGCAGGAGCAGTGCACAGAGGTGTCCCCAGAC
CCCTGTGCTCTAGTCTGTGCAAGCTGGAGGATGGTTGTTGGCTCCCCGGCCGGCTGGCTCCAGTGTGCTGG
GCGATGAGCTGCTTCTGCCAAACTGCCCCCCCAGCCGGAAAGTGCCTTCCGCAAGCTGGGCCACTGGAGGCC
AGGACTCACTCTACAACACTGCCACCAACTACAGAGTCCTGCTTCTCCCCCGCGAGGAGGCCAGCCCCCTGCAAGG
ACTGCCAGCCACTCTGCCACCAACTACAGAGTCCTGCTTCTCCCCCGCGAGGAGGCCAGCCCCCTGCAAGG
GGGTGGTGTCTTAGATGAGGATGAGGCAGAGCCAGAGGAACAG**TGA**CCCCACATCATGCCCTGGCAGTGGCATGCA
TCCCCCGGCTGCTGCCAGGGGAGGCCCTGTGCCCCAAGTGTGGGCTCAAGGCTCCAGCAGAGCTCCACAGCC
TAGAGGGCTCTGGGAGCGCTCGCTTCTCCGTTGTGTTTGATGAAAGTGTGTTGGAGAGGGAGGGCTG
GGCTGGGGCGCATGTCCTGCCCTCACTCCGGGCTTGCCGGGGCTTGCCGGGGCTCTGGGCATGGCTACA
GCTGTGGCAGACAGTGATGTTCATGTTCTTAAATGCCACACACATTTCTCCTCGGATAATGTGAACCACTA
AGGGGTTGTGACTGGCTGTGAGGGTGGGTGGAGGGGGCCAGCAACCCCCCACCCTCCCCATGCCCTCTC
TCTTCTCTGCTTTCTCTCACTCCGAGTCCATGTGCACTGCTGTTGATAGAATCACCCCCCACCCTGGAGGGCTGG
CTCTGCCCTCCGGAGCCTATGGGTGAGGCCCTCAAGGGCCCTGCCAGCTGGGCTCGTGTGCTTCT
ATTCAACCTCTCCATGTCCTAAATCTCCCTTTCTTCTAAAGACAGAAGGTTGGTCTGTTCTGTTCTCAGTC
GGATCTTCTCTCTGGGAGGCTTGGAAATGATGAAAGCATGTACCCCTCCACCCCTTCTGGCCCCCTAATGG
GGCCTGGGCCCTTCCCAACCCCTCTAGGATGTGCGGGCAGTGTGCTGGCCTCACAGCCAGCCGGCTGCC
ATTCAAGCAGAGCTCTGAGCGGGAGGTGGAAGAAAGGATGGCTCTGGTGTGCCACAGAGCTGGGACTTCATGTT
CTCTAGAGAGGGCCACAAGAGGGCACAGGGTGGCCGGAGTTGTCAGCTGATGCTGCTGAGAGGGAGGAAT
TGTGCCAGTGAAGTGAAGACTCATGAGGGAGTGTCTTCTTGGGAGGAAAGAAGGTAGAGCCTTCTGTCTGAAT
GAAAGCCAAGGCTACAGTACAGGGCCCCCAGCCAGGGTGTAAATGCCACGTAGTGGAGGCCTCTGGCAG
ATCCCTGCATCCAAGGTCACTGGACTGTACGTTTATGGTTGGGAAGGGTGGGTGGCTTATAAGAATTAAAGGC
CTTGTAGGCTTGGCAGGTAAGAGGGCCAAGGTAAGAACAGAGGCCAACAGCATTCTATATATAAGT
GGCTCATTAGGTGTTATTTGTTCTATTAAAGAATTGTTTATTAAATAAATAAAATCTTGAAATCT
AAAA



22/249

FIGURE 22

MFLATLSFLLPFAHPFGTVSCEYMLGSPLSSLAQVNLSPLSHPKVHMDPNYCHPSTSLHLCS
LAWSFTRLLHPPLSPGISQVVKDHVTKPTAMAQGRVAHLIEWKGWSKPSDSPAALSAFSSY
SDLSEGEQEAFRAAGVAEQFAIAEAKLRAWSSVDGEDSTDSDYDEDFAAGGMDTDMAGQLPLG
PHLQDLFTGHRFSRPVRQGSVEPESDCSQTVPSPDTLCSSLCSLEDGLLGSPARLASQLLGDE
LLLAKLPPSRESAFRSLGPLEAQDSLYNSPLTESCLSPAEEEPAPCKDCQPLCPPLTGSWER
QRQASDLASSGVVSLDEDEAEPEEQ

Signal peptide:

amino acids 1-15

Casein kinase II phosphorylation site.

amino acids 123-127, 128-132, 155-159, 162-166, 166-170, 228-232,
285-289, 324-328

Tyrosine kinase phosphorylation site.

amino acids 44-52

N-myristoylation site.

amino acids 17-23, 26-32, 173-179

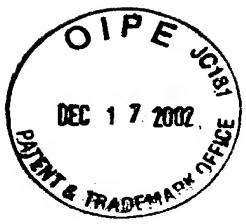
Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 11-22



FIGURE 23

GGTCCTGGCGCTGTTACACAAGCAAGATAAGCCAGCCCCACCTAATTTGTTCCCT
GGCACCCCTCCTGCTCAGTGCAGACATTGTACACTTAACCCATCTGTTCTAATGCACGA
CAGATTCCTTCAGACAGGACAACGTGATATTCAGTCAGTTCTGATTGTAAATACCTCCTAAG
CCTGAAGCTTCTGTTACTAGCCATTGTGAGCTTCAGTTCTCATCTGCAAATGGGCATAA
TACAATCTATTCTGCCACATCAAGGGATTGTTATTCTTAAAAAAACCAATACCAAAG
AAGCCTACA**ATGTTGGCCTAGCCAAAATTCTGTTGATTCACGTTGTTTATTCACTTCT**
ATCGGGGAGCCATGGAAAAGAAAATCAAGACATAAACACACAGAACATTGAGAAGTTT
TTAAAACAATGGAAAATAAACCTATTTCTTGAAAGTGAAGCAAACCTAAACTCAGATAAA
GAAAATATAACCACCTCAAATCTCAAGGCGAGTCATTCCCCTCCTTGAATCTACCCAAACAA
CAGCCACGGAATAACAGATTCTCCAGTAACTCATCAGCAGAGCATTCTGGCAGTCTAA
AACCCACATCTACCATTCCACAAGCCCTCCCTGATCCATAGCTTGTAAAGTGCCT
TGGAATGCACCTATAGCAGATGAAGATCTTGCCATCTCAGCACATCCAAATGCTACACC
TGCTCTGTCTTCAGAAAACCTCACTGGTCTTGGTCAATGACACCGTGAAAACCTCTGATA
ACAGTTCCATTACAGTTAGCATCCTCTTCAGAACCAACTTCTCCATCTGTGACCCCCCTG
ATAGTGGAACCAAGTGGATGGCTTACACAAACAGTGAAGCTCAGTGGTTACCCCTTA
TCAAGAAAAACAACTCTACAGCCTACCTAAAATTCAACAAATAATTCAAACCTTTCAA
ATACGTCAGATCCCCAAAAGAAAATAGAAATACAGGAATAGTATTGGGGCCATTAGGT
GCTATTCTGGGTGCTCATGCTTACTCTTGCTGGCTACTTGTGTGGAAAAGGAAAAC
GGATTCTTCCATGGCAGCTTATGACGACAGAAATGAACCAAGTCTGCGATTAGACA
ATGCACCGAACCTTATGATGTGAGTTGGAAATTCTAGCTACTACAATCCAACCTTGAAT
GATTGCCATGCCAGAAAGTGAAGAAAATGCACGTGATGGCATTCTATGGATGACATACC
TCCACTTCGTACTCTGT**TAGA**ACTAACAGCAAAAGGCGTAAACAGCAAGTGTCTA
CATCCTAGCCTTGACAAATTCTTCAAAAGGTTACACAAATTACTGTACGTGGAT
TTTGTCAAGGAGAATCATAAAAGCAGGAGACCAGTAGCAGAAATGTAGACAGGATGTATCAT
CCAAAGGTTTCTTCTTACAATTGGCCATCCTGAGGCATTACTAAGTAGCCTTAATT
TGTATTCTAGTATTTCTTAGTAGAAAATTTGTGGAATCAGATAAAACTAAAAGATT
TCACCATTACAGCCTGCCTCATAACTAAATAAAAAATTATTCCACCAAAAAATTCTAAA
ACAATGAAGATGACTCTTACTGCTCTGCCTGAAGCCCTAGTACCAATTCAAGATTGCAT
TTCTTAAATGAAAATTGAAAGGGTGTGTTAAAGAAAATTGACTAAAGCTAAAAGAG
GACATAGCCCAGAGTTCTGTTATTGGAAATTGAGGCAATAGAAATGACAGACCTGTATT
TAGTACGTTATAATTCTAGATCAGCACACACATGATCAGCCACTGAGTTATGAAGCTGA
CAATGACTGCATTCAACGGGCCATGGCAGGAAAGCTGACCCCTACCCAGGAAAGTAATAGCT
TCTTAAAGTCTCAAAGGTTGGAAATTAACTGTCTTAATATATCTTAGGCTCAA
TTATTGGGTGCCTTAAAACCAATGAGAATCATGGT



24/249

FIGURE 24

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58732
><subunit 1 of 1, 334 aa, 1 stop
><MW: 36294, pI: 4.98, NX(S/T): 13
MLALAKILLISTLFYSLLSGSHGKENQDINTTQNIAEVFKTMENKPISLESEANLNSDKENI
TTSNLKASHSPPLNLPNNSHGITDFSSNSSAEHSLGSLKPTSTISTSPPPLIHSFVSKVPWNA
PIADEDLLPISAHPNATPALSSENFTWSLVNDTVKTPDNSSITVSILSSEPTSPSVTPLIVE
PSGWLTTNSDSFTGFTPYQEKTTLQPTLKFTNNSKLFPNTSDPQKENRNTGIVFGAILGAIL
GVSSLTLVGYLLCGKRKTDSFSHRRLYDDRNEPVLRLDNAPEPYDVSGNSSYYNPTLNDSA
MPSEENARDGIPMDDIPPLRTSV
```

Signal peptide:

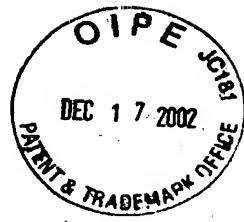
amino acids 1-23

Transmembrane domain:

amino acids 235-262

N-glycosylation site:

amino acids 30-34, 61-65, 79-83, 90-94, 148-152, 155-159,
163-167, 218-222, 225-229, 298-302, 307-311



25/249

FIGURE 25

AACAGGATCTCCTCTGCAGTCTGCAGGCCAGGACGCTGATTCCAGCAGCGCCTTACCGCGC
AGCCCAGAAGATTCACTATGGTGAAAATGCCCTCAATAACCCCTACCGCCGTGAAAAGGAGG
AGGCGCGCAAGACGTGGAGGCCCTCCTGAGCCGCACGGTCAGAACTCAGATACTGACCGGC
AAGGAGCTCCGAGTTGCCACCCAGGAAAAAGAGGGCTCCTCTGGGAGATGTATGCTTACTCT
CTTAGGCCTTCATTCATCTTGGCAGGACTTATTGTTGGAGCCTGCATTACAAGTACT
TCATGCCCAAGAGCACCATTTACCGTGGAGAGATGTGCTTTTGATTCTGAGGATCCTGCA
AATTCCCTCGTGGAGGAGAGCCTAACCTCCTGCCTGTGACTGAGGAGGCTGACATTGTGA
GGATGACAACATTGCAATCATTGATGTGCCTGTCCCCAGTTCTGTGATAGTGACCCCTGCAG
CAATTATTGACTTTGAAAAGGAAATGACTGCTTACCTGGACTTGTGCTGGGAACACTGC
TATCTGATGCCCTCAATAACTTCTATTGTTATGCCTCCAAAAAATCTGGTAGAGCTTTGG
CAAACGGCGAGTGGCAGATATCTGCCTCAAACCTATGTGGTCGAGAAGACCTAGTTGCTG
TGGAGGAAATTCTGATGTTAGTAACCTTGGCATCTTATTTACCAACTTGCAATAACAGA
AAGTCCTCCGCCTCGTCGCAGAGACCTTGTGGCTGGGTTCAACAAACGTGCCATTGATAA
ATGCTGGAAGATTAGACACTTCCCCAACGAATTATTGTTGAGACCAAGATCTGTCAAGAGT
AAGAGGCAACAGATAGAGTGCCTTGGTAATAAGAAGTCAGAGATTACAATATGACTTAA
CATTAAGGTTATGGGATACTCAAGATATTACTCATGCATTACTCTATTGCTTATGCTTT
AAAAAAAGGAAAAAAACTACTAACCAACTGCAAGCTCTGTCAAATTAGTTAAT
TGGCATTGCTTGTGTTGGAAACTGAAATTACATGAGTTTCATTTCTTGCATTTATAG
GGTTAGATTCTGAAAGCAGCATGAATATATCACCTAACATCCTGACAATAAATTCCATCC
GTTGTTTTTGTGTTGTTGTTCTTTCTTTAAGTAAGCTCTTATTGATCTTATG
GTGGAGCAATTAAAATTGAAATATTAAATTGTTGAACTTTGTGAAATTGTGAAATATA
TCAGATCTCAACATTGTTGGTTCTTTGTTCTTTCTTTAAGTAAGCTCTTATTGATCTTATG
AATTACATCTTGCAGTTCTGTTAGGTGCTCTGTAATTAAACCTGACTTATATGTGAACAAATT
TTCATGAGACAGTCATTTAACTAATGCAGTGATTCTTCTCACTACTATCTGTATTGTGG
AATGCACAAAATTGTGTAGGTGCTGAATGCTGTAAGGAGTTAGGTTATGAATTCTACAA
CCCTATAATAATTACTCTATACAAAAA



26/249

FIGURE 26

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58828
<subunit 1 of 1, 263 aa, 1 stop
<MW: 29741, pI: 5.74, NX(S/T): 1
MVKIAFNTPTAVQKEEARQDVEALLSRTVRTQILTGKELRVATQEKEGSSGRCMMLLGLSF
ILAGLIVGGACIYKYFMPKSTIYRGEMCFFDSEDPANSLRGGEPNFLPVTEEADIREDDNIA
IIDVPVPSFSDSDPAIIHDFEKGMTAYLDLLLGNCYLMPLNTSIVMPPKNLVELFGKLASG
RYLPQTYVVREDLVAVEEIRDVSNLGIFIFYQLCNNRKSFRRLRRRDLLLGFNKRAIDKCWKIR
HFPNEFIVETKICQE
```

Type II transmembrane domain:

amino acids 53-75

N-glycosylation site.

amino acids 166-170

Casein kinase II phosphorylation site.

amino acids 35-39, 132-136, 134-138

N-myristoylation site.

amino acids 66-72, 103-109

Prokaryotic membrane lipoprotein lipid attachment site.

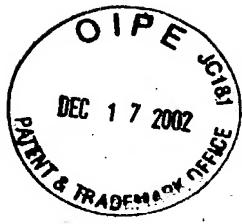
amino acids 63-74



27/249

FIGURE 27

GGAGGAGGGAGGGCGGGCAGGCAGCCCAGAGCAGCCCCGGGACCCAGCACGGACTCTCT
CTTCCAGCCCAGGTGCCCTTCACTCTCGCTCCATTGGCGGGAGCACCCAGTCCTGTACGCC
AAGGAACCTGGTCCTGGGGCACCATGGTTGGCGGGCAGCCCCAGCCTCCTCATCCTTCTG
TTGCTGCTGCTGGGGTCTGTGCCTGCTACCGACGCCGCTCTGTGCCCTGAAGGCCACGTT
CCTGGAGGATGTGGCGGGTAGTGGGGAGGCCGAGGGCTGTCGGCCTCCTCCCCGAGCCTCC
CGCCACCCCTGGACCCCGGCCCTCAGCCCCACATCGATGGGGCCCAAGCCCACAACCCTGGGG
GGCCCATCACCCCCAACCAACTTCCTGGATGGATAGTGGACTTCTCCGCCAGTACGTGAT
GCTGATTGCTGTGGTGGGCTCCCTGGCCTTCTGCTGATGTTCATCGTCTGTGCCGCCGGTCA
TCACCCGGCAGAACAGCAGAACAGCAGGCCCTCGGCCTATTACCCATCGCCTTCCCCAAGAACAGTAC
GTGGACCAGAGTGACCGGGCCGGGGCCCCGGGCCTTCAGTGAGGTCCCCGACAGAGCCCC
CGACAGCAGGCCGAGGAAGCCCTGGATTCCCTCCGGCAGCTCCAGGCCGACATCTGGCCG
CCACCCAGAACCTCAAGTCCCCCACCAAGGGCTGCACTGGCGGTGGGACGGAGGCCAGGATG
GTGGAGGGCAGGGCGCAGAGGAAGAGGAGAACGGCAGCCAGGAGGGGACCAGGAAGTCCA
GGGACATGGGTCCCAGTGGAGACACCAGAGGCCAGGAGGAGCCGTGCTCAGGGTCCTTG
AGGGGCTGTGGTGGCCGGTGAGGCCAAGGGAGCTGGAAAGGGTCTCTCTGTTAGCCCAG
GAAGCCAGGGACCAGTGGGTCCCCCGAAAGCCCTGTGCTTGAGCAGTGTCCACCCAG
TGTTAACAGTCCTCCGGCTGCCAGCCCTGACTGTCGGGCCCCAAGTGGTCACCTCCCC
GTGTATGAAAAGGCCTTCAGCCCTGACTGCTTCCTGACACTCCCTCCTGGCCTCCCTGTGG
TGCCAATCCCAGCATGTGCTGATTCTACAGCAGGCAGAAATGCTGGTCCCCGGTCCCCGG
GGAATCTTACCAAGTGCCATCATCCTCACCTCAGCAGCCCCAAAGGGCTACATCCTACAGC
ACAGCTCCCTGACAAAGTGAGGGAGGGCACGTGTCCCTGTGACAGCCAGGATAAAACATCC
CCCAAAGTGCTGGGATTACAGGCGTGAGGCCACCGTGCCCGGCCAAACTACTTTAAACACA
GCTACAGGGTAAATCCTGCAGCACCCACTCTGAAAATACTGCTTTAATTTCTGAAGG
TGGCCCCCTGTTCTAGTTGGTCCAGGATTAGGGATGTGGGTATAGGGCATTAAATCCTC
TCAAGCGCTCTCCAAGCACCCCCGGCCTGGGGTGAGTTCTCATCCGCTACTGCTGCTGG
GATCAGGTTGAATGAATGGAACCTTCCTGTCTGGCCTCAAAGCAGCCTAGAAGCTGAGGG
GCTGTGTTGAGGGGACCTCCACCCCTGGGAAGTCCGAGGGCTGGGGAAAGGGTTCTGACG
CCCAGCCTGGAGCAGGGGGCCCTGGCCACCCCTGTTGCTCACACATTGTCTGGCAGCCTG
TGTCCACAATATTGTCAGTCCTGACAGGGAGCCTGGCTCCGTCTGCTTAAAGGAGGCT
CTGGCAGGAGGTCCCTCCCCCATCCCTCCATCTGGGCTCCCCAACCTCTGCACAGCTCT
CCAGGTGCTGAGATATAATGCACCAGCACAATAACCTTATTCCGGCCTGAAAAAAAAGA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGA



28/249

FIGURE 28

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58852
><subunit 1 of 1, 283 aa, 1 stop
><MW: 29191, pI: 4.52, NX(S/T): 0
MVSAAAPSLLLLLLLGSVPATDARSVPLKATFLEDVAGSGEAEGSSASSPSLPPPWTPAL
SPTSMGPQPTTLGGPSPPTNFLDGVDFRQYVMLIAAVGSLAFLLMFIVCAAVITRQKQKA
SAYYPSSFPKKKYVDQSDRAGGPRAFSEVPDRAPDSRPEEALDSSRQLQADILAATQNLKSP
TRAALGGGDGARMVEGRGAEEEKGSQEGDQEVAQGHGPVETPEAQEEPCSGVLEGAVVAGE
GQGELEGSLLAQEAQGPVGPPESPCACSSVHPSV
```

Signal peptide:

amino acids 1-25

Transmembrane domain:

amino acids 94-118

N-myristoylation site.

amino acids 18-24, 40-46, 46-52, 145-151, 192-198, 193-199,
211-217, 238-244, 242-248



29/249

FIGURE 29

GTGGACTCTGAGAAGCCCAGGCAGTTGAGGACAGGAGAGAGAAGGCTGCAGACCCAGAGGGA
GGGAGGACAGGGAGTCGGAAGGAGGGACAGAGGAGGGCACAGAGACGCAGAGCAAGGGCG
GCAAGGAGGGAGACCCCTGGTGGAGGAAGACACTCTGGAGAGAGAGGGGCTGGCAGAGTG
AAGTTCCAGGGGCCCTGGCCTGCCTCTGCTGGCCCTGCCTGGCAGTGGGAGGCTGG
CCCCCTGCAGAGCGGAGAGGAAAGCACTGGACAAATATTGGGAGGCCCTGGACATGGCC
TGGGAGACGCCCTGAGCGAAGGGTGGAAAGGCCATTGGCAAAGAGGCCGGAGGGCAGCT
GGCTCTAAAGTCAGTGAGGCCCTGGCCAAGGGACCAGAGAACAGTGGCACTGGAGTCAG
GCAGGTTCCAGGCTTGGCGCAGCAGATGCTTGGCAACAGGGTGGGAAGCAGCCCAG
CTCTGGAAACACTGGCACGAGATTGGCAGACAGGCAGAAGATGTCATTGACACGGAGCA
GATGCTGTCCGGCTCCTGGCAGGGGTGCCCTGGCACAGTGGTGGCTGGAAACTCTGG
AGGCCATGGCATCTTGGCTCTCAAGGTGGCCTGGAGGCCAGGGCAATCCTGGAG
GTCTGGGACTCCGTGGTCCACGGATAACCCGAAACTCAGCAGGCAGCTTGGAAATGAAT
CCTCAGGGAGCTCCCTGGGTCAAGGAGGAATGGAGGGCCACCAAACCTTGGACCAACAC
TCAGGGAGCTGTGGCCAGCCTGGCTATGGTCAGTGAGAGGCCAGCAACCAGAATGAAGGGT
GCACGAATCCCCACCATCTGGCTCAGGTGGAGGCTCCAGCAACTCTGGGGAGGCAGCGC
TCACAGTCGGCAGCAGTGGCAGCAATGGTACAACAACATGGCAGCAGCAGTGG
TGGCAGCAGCAGTGGCAGCAGCAGTGGCAGCAGCAGTGGCAGCAGCAGTGGCAGCAG
GTGGCAGCAGTGGCAACAGTGGTGGCAGCAGAGGTGACAGCGGCAGTGGAGTCCTCCTGG
TCCAGCACC GGCTCCTCCGGCAACCACGGTGGAGCGGGAGGAAATGGACATAAAC
CGGGTGTAAAAGCCAGGGAAATGAAGCCGGAGCGGGGAATCTGGGATTAGGGCTTCA
GAGGACAGGGAGTTCCAGCAACATGAGGGAAATAAGCAAAGAGGGCAATGCCCTCTGG
GGCTCTGGAGACAATTATCGGGGCAAGGGTCAGCTGGGAGGTGACGCTGT
TGGTGGAGTCATACTGTGAACTCTGAGACGTCTGGATGTTAACCTTGACACTTCT
GGAAGAATTAAATCCAAGCTGGTTCATCAACTGGATGCCATAAACAGGACCAGAGA
AGCTCTCGCATCCGTGACCTCCAGACAAGGAGCCACCAGATTGGATGGAGCCCCACACT
CCCTCCTAAACACCACCCCTCTCATCACTAATCTCAGCCCTGCCCTGAAATAACCTTA
GCTGCCCAACAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAA



30/249

FIGURE 30

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59212
><subunit 1 of 1, 440 aa, 1 stop
><MW: 42208, pI: 6.36, NX(S/T): 1
MKFQGPLACLLLALCLGSGEAGPLQSGEESTGTNIGEALGHGLGDALSEGVGKAIGKEAGGA
AGSKVSEALGQGTREAVGTGVRQVPGFAADALGNRVGEAAHALGNTGHEIGRQAEDVIRHG
ADAVRGSWQGVPGHSGAWETSGGHGIFGSQGGLGGQQGNPGGLGTPWVHGYPGNSAGSFGM
NPQGAPWGQGGNGGPPNFGTNTQGAVAQPGYGSVRASNQNEGCTNPPPSGSGGSSNSGGGS
GSQSGSSGSGSNGDNNNGSSSGSSSGSSGGSSGGSSGSGSRGDSGSESSW
GSSTGSSSGNHGGGGNGHKGCEKPGNEARGSGESGIQGFRGQGVSSNMREISKEGNRL
GGSGDNYRGQGSSWGSGGDAVGGVNTVNSETSPGMFNFDTFWKNFKSKLGFINWDAINKDQ
RSSRIP
```

Signal peptide:

amino acids 1-21

N-glycosylation site.

amino acids 265-269

Glycosaminoglycan attachment site.

amino acids 235-239, 237-241, 244-248, 255-259, 324-328, 388-392

Casein kinase II phosphorylation site.

amino acids 26-30, 109-113, 259-263, 300-304, 304-308

N-myristoylation site.

amino acids 17-23, 32-38, 42-48, 50-56, 60-66, 61-67, 64-70,
74-80, 90-96, 96-102, 130-136, 140-146, 149-155, 152-158,
155-161, 159-165, 163-169, 178-184, 190-196, 194-200, 199-205,
218-224, 236-242, 238-244, 239-245, 240-246, 245-251, 246-252,
249-252, 253-259, 256-262, 266-272, 270-276, 271-277, 275-281,
279-285, 283-289, 284-290, 287-293, 288-294, 291-297, 292-298,
295-301, 298-304, 305-311, 311-317, 315-321, 319-325, 322-328,
323-329, 325-331, 343-349, 354-360, 356-362, 374-380, 381-387,
383-389, 387-393, 389-395, 395-401

Cell attachment sequence.

amino acids 301-304



31/249

FIGURE 31

GACCGGTCCCTCCGGTCTGGATGTGCGGACTCTGCTGCAGCGAGGGCTGCAGGCCGCCGGGGCTCACC
TGCCTGGCTGGTGGAGTTCTCTCCTTGCTGACCATGTTGTCCTTGCTGAATATTACCGGGACATCTTCA
CTCTCCTGCTGCGCTGCACCGGAGCTGGTGTGCGAGGAGACTGAGGGGAAGATGTGTTCTGAACAAGC
TGCTGCTACTTGCTGCTGGCTGGCTTCCAGATCCCACAGTCCCCTGAGGACTGTTCTTCTGAAAGAGG
GTCCTCATATGCCTTGAGGTGGACACAGTAGCCCCAGAGCATGGCTTGACAATGCGCTTGTTGGACCAGC
AGCTGCTACACCTGCTGCCCTACATCGAGAGCTCCGAAACTGCTCGCTCGTGGGTGTCAGGAGTAGTG
GACGGAGTGGGGCTTCATGAGGAAAATCACCCCCACCACTACCACCAGCCTGGGAGCCCAGCCTCCAGACCA
GCCAGGGGCTGCAGGACAGCTGCCCAAGGCCCTTTTCCACAACCAAGCAGCCCTCCTGCGCCGACCGTAGAGT
TCGTGGCAGAAAAGAATTGGATCAAACACTGTGTCACACATCAAGGCTACACTGGTGGCAGATCTGGTGCAGCAG
CAGAGTCACCTCTCCAAGAGCAGCTGGTACACAGGGAGAGGAAGGGGAGACCCAGCCAGCTGTTGGAGATCT
TGTGTTCCAGCTGTGCCCTCACGGGGCCCAAGGATTGGCCCTGGGGGGAGTTCTGTCAAAGGAAGAGCCTG
GGGCTGTGCGGGCGCTGCTCCAGAGGAGACCCGGCAGCCGTTCTGAGCAGTGCAGAGAACATTGCTGTGGGC
TTGCAACAGAGAAGCCTGTGCTGGCTGTCAGCAACATCACGACTGATCAGGAGGGAGGTGAAAGCAGCAG
TGAGTCGCACACTTCGAGCCCAGGGCTCTGAAACCTGTCAGGCCGGGGAGCGGAGGGCTGCTCCGCGCC**TGAC**
GTGCTCTCCTGGCGTGGGGCACGGGACCCCTGACCGAGGGAGTCTCCCCAGAGCATCTGAAACAGCTCTAGGC
CAGCTGGGCCAGACGCTGCGGTGCCAGTCCCTGTCAGCAGCATCTGCAAAGTGCCTGTG
GAGTTAGCTCCCTCTCGTTGCAAGATCAAATTCTATCCTAGGGCCCCCGCACAGTACAGGCTGGAGAGAGG
CAGGCTCGAAGGCTCTGCACATGCTGCTTCTTGCAAGGAAGAGACTTCAGGGGGCTTCCGCTGCAGCTG
CTGCTGAGCCAAGAAATGTGGGCTCTGGCAGACACAAGGCAAAAGGGAGTGGGACTTGTGCTATTCTTGCTA
CGGGAGCTGGTGGAGAAGGGTCTGATGGGACGGATGGAGATAGAGGCTGCTGGCAGCCTCCACCAGGCCAG
TGGCCAGGGGACTTGTGAGAAGAATTGCAACACTGTCTAATCTGTTCTAGCCGAGCCCCACCTGCCAGAACCC
CAGCTAAGAGGCTGTGAGTGGTGCAGCCAAACGGGCACTGTGCTGGCCCAGAGCTAGGGCTGAGAAGTGGCC
CTGCCCTGGCATTGCAACCAGAACCCCTGGACCCCCGCCCTCACGAGGAGGGCCAAGTGCCAATGCAGACCCCTCAC
TGGTTGGGTGAGCTGGCTACAGTCAGACTCCTGCTTAAGGGTGTACTGCCCTGGCATCCCACCAGCGA
ATCCTAGAGGAAGGAGAGTGGCCTGATTGGGATTATGGCAGAAAAGTCAGAGATGCCAGTCTGGAGTAGAA
GAGGTGGTTTGTCTGGATACTAAATGAAATGAGGTGTGGCTTGTCAACACAGAACATTCAAGCCT
CATTTGCTATCCCAGCATCTCTAAACACTTGTAGTCTTGGAAATTGACAGAGGCAAATGACTCCTGCTTAAC
TTATGAAGAAAAGTTAAACATGAATCTTGGGAGTCTACATTCTTATCACCAGGAGCTGGACTGCCATCTCCTT
ATAAATGCCAACACAGGCCGGCTGGTGGCTCATGCCCTGTAATCCCAGCACTTGGAGAGGCTGGCG
GACTGCCCTGAGGTCAAGGCAAGGACGCCCTGCCAACATGCCAAACCCCCATCTCTACTAAAAAATAAAAAA
TTATTAGCTGGGATGGTGGTGTGCTGCTGTAATCCCAGCTACAGGAGGATGAGGAGGAGACCTGCTTGAAC
CTGGAGGTGGAGGTTGAGCTGAGCGAGGTCGACCACTGCACTCCAGTCTGGGTAACAGAGCGAGACTTTCTAG
AAAAAGCTAACAAACAGATAAGGTAGGACTCAACCAACTGAAACCTGACTTTCCCTGTAACCTCAGCCCTG
TGCAGGTAGTAAACCTCTGAGACCTCTCCCTGACCAAGGGACCAAGCACAGGGCATTTAGAGCTTTAGAATAAA
CTGGTTTCTTAAAAAAGGGCTTTATTAAAATTCTCCCCACAGATGGCTCTGCAATCTGCCACAGCTC
TGGGGCGTGTCTGTAGGGAAAGGCCCTGTTCCCTGAGGCGGGCTGGGCTTGTCCATGGGTCGGAGCTG
GCCGTGCTGGGCCCTGGCGTGTCTAGCTGCTTGTGCGGGCACAGAGCTGCCGGTCTGGGGCACCGGG
AGCTAACAGAGCAGGCTCTGGTCAGGGTGGAGGCTGTCTCTAACCGACACCCCTGAGGTGCTCCTGAGATGCTG
GGTCCACCCCTGAGTGGCACGGGAGCAGCTGTGGCCGGTGTCTCTCYTAGGCCAGTCTGGGAAACTAACGCTC
GGGCCCTCTTGCAAAAGACCGAGGATGGGTGGGTGTGGGGGACTCATGGGAATGCCCTGAGGAGCTACGTGT
GAAGAGGGCGCCGGTTGTTGGCTGCAGGGCCTGGAGGCCCTCTCCTGAGGCTCAGTTCCCTTCCGTCTA
ATGAAGAACATGCCGTCTGGTCTCAGGGCTATTAGGACTTGGCTCAGGAAGTGGCTTGGACGAGCGTCAT
GTTATTTCACAACCTCTCTGGCACGTTGGCTGGCACGTCTGGGAATGCCCTGAGGAGGCTGGGAGGCGCCGGAGGG
GTCGGCGTGGGAGTGCAGCCAGAGGGGGGGAGACGTGCGCCTGGGGTGGAGGGAGGCGCCGGAGGG
CCTCACAGGAAGTTGGCTCCCGCACCACAGGCAGGGCGGGCTCCGCCGCCGCCACCACCGTCCAGG
GGCCGGTAGACAAAGTGGAGTGCAGCAGGGCTCCACCAGCACGAACAGCCGGTGCAGC
TCGTCCGCCAGCTGGAAGCAGGCCGTCCACCAGCACGAACAGCCGGTGCAGC



32/249

FIGURE 32

MCFLNKLLLLAVLGWLFQIPTVPEDLFFLEEGPSYAFEVDTVAPEHGLDNAPVVDQQLLYTC
CPYIGELRKLLASWVGSSGRSGGFMRKITPTTTSLGAQPSQTSQLQAQLAQAFFHNQPP
SLRRTVEFVAERIGSNCVKHIKATLVADLVRQAESLLQEQLVTQGEEGGDPAQLLEILCSQL
CPHGAQALALGREFCQRKSPGAVRALLPEETPAAVLSSAENIAVGLATEKACAWLSANITAL
IRREVKAASRTLRAQGPEPAARGERRGCSRA

Signal peptide:

amino acids 1-18

N-glycosylation site.

amino acids 244-248

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 89-93

Casein kinase II phosphorylation site.

amino acids 21-25, 167-171, 223-227

N-myristoylation site.

amino acids 100-106, 172-178, 207-213

Microbodies C-terminal targeting signal.

amino acids 278-282



33/249

FIGURE 33

TCCCTTGACAGGTCTGGTGGCTGGTCGGGGTCACTGAAGGCTGTCTGATCAGGAAACTG
AAGACTCTCTGCTTTGCCACAGCAGTCCCTGCAGCTCCTGAGGTGTGAACCCACATCCC
TGCCCCCAGGGCCACCTGCAGGACGCCGACACCTACCCCTCAGCAGACGCCGGAGAGAAATG
AGTAGCAACAAAGAGCAGCGGTAGCAGTGGTGTGATCCTCTTGCCCTCATCACCATCCT
CATCCTCTACAGCTCCAACAGTGCCAATGAGGTCTTCATTACGGCTCCCTGCGGGGCCGTA
GCCGCCGACCTGTCAACCTCAAGAAGTGGAGCATTGACGGCTATGCCCCATTCTCGGC
AACAAAGACACTGCCCTCTCGGTGCCACCAGTGTGATTGTAGCAGCTCCAGCCACCTGCT
GGGCACCAAGCTGGGCTTGAGATCGAGCGGGCTGAGTGTACAATCCGATGAATGATGCAC
CCACCACTGGCTACTCAGCTGATGTGGCAACAAGACCACCTACCGCGTGTGGCCATTCC
AGTGTGTTCCCGTGTGAGGAGGGCCCAGGAGTTGTCAACCGGACCCCTGAAACCGTGT
CATCTCTGGGGCCCCCGAGCAAGATGCAAGAGCCCCAGGGCAGCCTCGTGCCTGTGATCC
AGCGAGCGGGCTGGTGTCCCCAACATGGAAGCATATGCCGTCTCTCCGGCCGATGCGG
CAATTGACGACCTCTTCCGGGTGAGACGGCAAGGACAGGGAGAAGTCTCATTGTGGTT
GAGCACAGGCTGGTTACCATGGTGTGACGGCTGGAGTTGTGACCGACGTGATGTCTATG
GCATGGTCCCCCAACTACTGCAGCCAGCGGGCCCTCCAGCGCATGCCCTACCAACTAC
TACGAGCCAAGGGGCCGGACGAATGTGTACCTACATCCAGAATGAGCACAGTCGCAAGGG
CAACCACCACCGCTCATCACCGAGAAAAGGGTCTTCTCATCGTGGGGCCAGCTGTATGGCA
TCACCTTCTCCCACCCCTCTGGACCTAGGCCACCCAGCCTGTGGGACCTCAGGAGGGTCAG
AGGAGAACGCCCTCGCCAGCCCTAGGCCAGGGACCATCTCTGCCAATCAAGGCTTG
CTGGAGTGTCTCCAGCCAATCAGGGCTTGAGGAGGATGTATCCTCCAGCCAATCAGGGCC
TGGGAATCTGTTGGCAATCAGGGATTGGGAGTCTATGTGGTTAATCAGGGGTGTCTTC
TTGTGCAGTCAGGGCTGCGCACAGTCAATCAGGGTAGAGGGGTATTCTGAGTCATCTG
AGGCTAAGGACATGCTCTTCCCAGTGGCTGGGATAATGGGCTCTGTCCCAGGAGCTGGAACTTGGTGT
ATCACTCCCCACTCTGCTGGATAATGGGCTCTGTCCCAGGAGCTGGAACTTGGTGT
CCCCCTCAATTCCAGCACAGAAAGAGAGATTGTGTGGGGTAGAAGGCTGTCTGGAGGGCC
GGCCAGAGAATTGTGGGTTGTGGAGGTTGTGGGGCGGTGGGAGGTCCCAGAGGTGGGA
GGCTGGCATCCAGGTCTGGCTCTGCCCTGAGACCTGGACAAACCTCCCCCTCTGG
CACCTCTGCCACACCAGTTCCAGTGCAGGAGTCTGAGACCCCTTCCACCTCCCCTACAA
GTGCCCTGGGTCTGCTCTCCCCGTCTGGACCCCTCCAGCCACTATCCTCTGCTGGAGGCT
CAGCTCTTGGGGGTCTGGGTGACCTCCCCACCTCTGGAAAACCTTGGGTATTTC
GCAAACCTCTCAGGGTTGGGGACTCTGAAGGAAACGGGACAAACCTTAAGCTTTCT
TAGCCCCTCAGCCAGCTGCATTAGCTGGCTCTAAAGGGCAGGCCTCTTCTGCCCT
CTAGCAGGGAGGTTTCAACTGTTGGAGGCCCTTGGGTGCCCCCTTGTCTGGAGTCA
CTGGGGCTTCCAGGGTCTCCCTGACCCCTCTGTGCTCTGGATGGCTGTGGAGCTGT
ATCACCTGGGTCTGCTCCCTGGCTCTGTACGGCACTTATTAAAGCTGGGCTCAGTGG
GGTGTGTTGTCTCTGCTCTGGAGGCCCTGGAAGGAAAGGGCTTCAGGAGGAGGCTGTGA
GGCTGGAGGGACAGATGGAGGAGGCCAGCAGCTAGCCATTGCACACTGGGTGATGGGTGG
GGCGGTGACTGCCAGACTGGTTGTAAATGATTGTACAGGAATAAACACACCTACGC
TCCGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA



34/249

FIGURE 34

MSSNKEQRSAVFVILFALITILYLSSNSANEVFHYGSLGRSRRPVNLKKWSITDGYVPIL
GNKTLPSRCHQCVIVSSSSHLLGKLGPEIERAECTIRMNDAPTTGYSADVGNKTYRVVAH
SSVFRVLRRPQEJVNRTPETVFIFWGPPSKMQKPQGSLVRVIQRAGLVFPNMEAYAVSPGRM
RQFDDLFRGETGKDREKSHSWLSTGWFTMVIACHELCDHVHVYGMVPPNYCSQRPRLQRMPYH
YYEPKGPDECVTYIQNEHSRKGNHHRFITEKRVFSSWAQLYGITFSHPSWT

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 9-31 (type II)

N-glycosylation site.

amino acids 64-68, 115-119

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 50-54

Casein kinase II phosphorylation site.

amino acids 3-7, 29-33, 53-57, 197-201

Tyrosine kinase phosphorylation site.

amino acids 253-262

N-myristoylation site.

amino acids 37-43, 114-120, 290-294



SEARCHED SERIALIZED FILED

35/249

FIGURE 35

GTTCATAGTTGGCGTCTTCTAAAGGAAAAACACTAAAATGAGGAACCTAGCGGACCGGGAGCGACGCAGCTT
GAGGGAAGCATCCCTAGCTGTTGGCGCAGAGGGGCGAGGCTGAAGCCGAGTGGCCCGAGGGTGTCTGAGGGCTGG
GCCAAAGGTGAAAGAGTTCTAGAACAGCTCTGGAACCCATGAAGCTTGTGACATTTATACCGT
CTGAGGGTAGCAGCTCGAAACTAGAAGAAGTGGAGTGTGAGGGACGGCAGTATCTTTGTGACCGCTGGC
GCCCTATGGGACGTTGGCTTCAGACCTTGAGTACACCATGCTGCGTGGGACGATGACGGCGTGGAGAGGAATG
AGGCTGAGGTACACACTGGCTTGCCTCTAGCCACAGCAGGGCTGCTTGTACTGAACGAGGTCCCTCAG
GTCACCCTCAGCCTGCGTCCACCGTCCAGAAGGCCGGAGGCAGTGTGATCTGGGCTGCGTGGTGGAACCTCCA
AGGATGAATGTAACCTGGCGCTGAATGAAAGGAGCTGAATGGCTCCAGGACTGAGTGTCTGGGTGCTCATCACC
CACGGGACCCCTCGTCACTGCCTTAAACACACACTGTGGGACGGTACCCAGTGTGCCCCGGATGCCGCG
GGGCTGTGCCAGCGTGCAGCCACTGTGACACTAGCCAATCTCAGGACTCTAACGTTAGATGTGAGCACGTG
ATTGAAGTGGATGAGGAAACACAGCAGTCATTGCTGCCACCTGCGTGGAGAGCCACCCAAAGGCCAGGTCCGG
TACAGCGTCAAACAAGAGTGGCTGGAGGCCAGAGGTAACTACCTGATCATGCCCTCAGGGAACCTCCAGATT
GTGAATGCCAGCCAGGAGGACGAGGGCATGTACAAGTGTGAGCCTACAACCCAGTGAACCCAGGAAGTGAAC
TCGGGCTCCAGCGACAGGCTACGTGTGCGCGCTCCACCGCTGAGGCTGCCGATCATCTACCCCCCAGAGGGC
CAAACCATCATCGTCACCAAAGGCCAGAGTCTCATTCTGGAGTGTGAGGCTGAGGACCTCCACGGGTC
ACCTGGGCAAGGATGGCTCCAGGTGCTACCCGCTACACAAAGACCGCCTCCCTGCTGAGCAACCTCCTCATCGAC
ACCACCGAGGAGGACTCAGGCACCTACCGCTGCATGGCGACAATGGGTTGGCAGGCCAGGGTC
ATCCTCTACAATGTCAGGTGTTGAACCCCTGAGGTACCATGGAGCTATCCCAGCTGGTATCCCCTGGG
CAGAGTGCCAAGCTTACCTGTGAGGTGCGTGGGAACCCCCCGCCCTCCGTGCTGTGGCTGAGGAATGCTGTGCC
CTCATCTCCAGCCAGCGCCTCCGCTCTCCCGCAGGGCCCTGCGCTGCTCAGCATGGGCTGAGGACAG
GTCCTACAGTGCATGGCGAGAACGAGGTGGGAGCCTGGCTAGTCCAGCTGCGGACCTCCAGGCAAGC
ATAACCCCAAGGCTATGGCAGGATGCTGAGCTGGCTACTGGCACACCTCTGTATCACCCCTCAAACCTGGCAAC
CTGAGCAGATGCTGAGGGGGCAACCGCGCTCCCCAGACCCCAACGTCACTGGGGCTGCTTCCCAGTGT
CCAGGAGAGAAGGGGAGGGGGCTCCCGCCGAGGCTCCCATCATCTCAGCTGCCCGCACCTCCAAGACAGAC
TCATATGAACTGGTGTGGCGGCCCTCGGCATGAGGGCAGTGGCCGGGCGCCAATCCTCTACTATGTGGTGAAC
CGCAAGCAGGTACAAACATTCTGTGACGATGGGACCATCTCTGGCATTCCAGGCAACCCAGCAGGCGCTGAC
ACCAGACTTGCACCCGGAGCTTGTATGAAGTGGAGATGGCAGCTTACAACACTGTGCGGAGAGGCCAGACGCC
ATGGTACCTTCCGAACTGGACGGGCCAACCCAGATCATGGCAGCAAAGAGCAGCAGATCCAGAGAGAC
GACCCTGGAGGCCAGTCCCCAGAGCAGCAGCCAGACCACGGCCGCTCTCCCCCCCAGAACGCTCCGACAGG
CCCACCATCTCCACGGCTCCAGACCTCAGTGTACGTGACCTGGATTCCCCGTGGGAATGGTGGTTCCCAATC
CAGTCTTCCTGCTGAGTACAAGAAGCTAAAGAAAGTGGGAGACTGGATTCTGGCACCAGCGCCATCCCCCA
TCGGGCTGTCCGTGGAGATCACGGGCTAGAGAAAGGCACCTCTACAAGTTCTGGAGTCCGGGCTGTGAACATG
CTGGGGAGAGCAGGCCAGCGCCCCCTCTGGGCTTACGTGGTGTGGCTACAGCGGTGCGTGTACGAGGAG
CCCGTGGCAGGTCTTATACCTCACGGATGCGGTCAATGAGACCACCATCATGCTCAAGTGGATGTACATC
CCAGCAAGTAACAACACACCCAACTCATGGCTTTATATCTATTATCGACCCACAGACAGTGACAATGATA
GACTACAAGAAGGATATGGTGGAAAGGGGACAAGTACTGGCACTCCATCAGGCCACCTGAGCCAGAGACCTCCT
GACATTAAAGATGAGCAGTGTCTCAAGAAGGAGGGGAGAGCAGTGTGAGCAACGTGATCTGTGAGGACAAAGCT
CGGAAGTCTCTGGCCAGCGCTGGACTGGCCACCCCCAACCTCTGGGCCCCAACAGCGGCTTCTCTGAAAC
ATAGAGCGGGCGGTGGGACTGGGCCATGGTGGCTGCTCAGCAGGACCTGCCCCTATCTGATTGTGGGTGTC
CTGGGCTCATCGTCTCATCGTCACCTCATCCCCTCTGCTTGTGAGGGCTGGTCTAAGCAAAACAT
ACAACAGACCTGGGTTTCCTCGAAGTGGCCTCCACCCCTCTGCCCCTACTATGGTGCATTGGGAGGACTC
CCAGGCCACCGCCAGTGGACAGCCCTACCTCAGTGGCATCAGTGGACGGCCCTGTGCTAATGGGATCCACATG
AATAGGGCTGCCCTCGCAGTGGGCTACCGGCTAGAAGGCCCCAACCTCTGGGCCCCAACAGCGGAGCTTCAG
CAGCAGAGTGCACCCAGCAGCCTGCTGAGGGAGACCCATCTGGCAATGGATATGACCCCCAAAGTCACCA
ACGAGGGGCTCCAAGTCTAGCCCCAGAGGGCTCTTCTTATACACACTGCCCAGGACTCCACTCACAGCTG
CTGCAGCCCCATCACGACTGCTGCCAACGCCAGGAGCAGCTGCTGTGGCCAGTCAAGGGTGAGGAGAGCC
CCCGACAGTCTGTCTGGAGACAGTGTGGGACCCCTCCATTCTACTCAGGGCCCCATGCTGTGGCCTGTG
CCAGTGTGAAGAGGTGGACAGTCTGACTCCGCCAGTGGAGTGGAGGAGACTGGTCTCCCCAGCACCCCGTAGGG
GCCCTAGTGGAGACAGGAAACCTGGGATGCAGCTCTCCCCGGGGCAACTGGTGTGCTTGTCTTGGAAAC
CTCACAAATTTAGCAGAAGCTGATATCCCAGAAAGACTATATATTGTTTTTTTAAAGAAGAAAA
AGAGACAGAGAAATTGGTATTATTTCTATTATAGCCATATTATATGACTGTAAATAATGTA
TATGTTTATAATTCTGGAGAGACATAAGGAGTGTCTACCGGTTAGGGTGGAGAGGGAAAATAAAGAAGCTGCCA
CTAACAGGAGTCACCCAGGAAGCACCAGCACAGGCTGGCGGGACAGACTCCTAACCTGGGGCTCTGCAGTG
GCAGGCGAGGCTGCAGGAGGCCACAGATAAGCTGGCAAGAGGAAGGATCCAGGCACATGGTCTCATCAGAGCA
TGAGGGAAACAGCAAGGGGCACGGTATCACAGCCTGGAGACACCCACAGATGGCTGATCCGGTGTACGGGAA
ACATTTCCTAAGATGCCCATGAGAACAGACCAAGATGTGACAGCACTATGAGCATTAAAAACCTTCCAGAAT
CAATAATCCGTGGCAACATATCTGTAAAAACAAACACTGTAACTTCTAAATAATGTTAGTCTCCCTGTAAAA



36/249

FIGURE 36

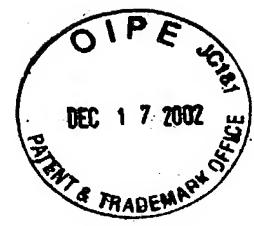
MLRGTMATWRGMRPEVTLACLLLATAGCFADLNEVPQVTVPASTVQKPGGTUILGCVVEPP
RMNVTRWLNGKELNSSDDALGVLITHGTLVITALNNHTVGRYQCVARMPAGAVASVPATVTL
ANLQDFKLDVQHVIEVDEGNTAVIACHLPESHPKAQVRYSVKQEWLEASRGNYLIMPSGNLQ
IVNASQEDEGMYKCAAYNPVTQEVKTSGSSDRLRVRRSTAEEAARIIYPPEAQTIIVTKGQSL
ILECVASGIPPPRVTWAKDGSSVTGYNKTRFLSNLLIDTTSEEDSGTYRCMADNGVGQPGA
AVILYNVQFEPPEVTMELSQLVIPWGQSAKLTCEVRGNPPPSVLWLRNAVPLISSQRLRLS
RRALRVLSMGPEDEGVYQCMAENEVGSAAVVQLRTSRPSITPRLWQDAELATGTPPVSPSK
LGNPEQMLRGQPALPRPPTSVGAPSKCPGEKGQGAPAEAPIILSSPRTSKTDSYELVWRPR
HEGSGRAPILYYVVKHRKQVTNSSDDWTISGIPANQHRLTLTRLDPGSLYEVEMAYNCAGE
GQTAMVTFRGRRPKPEIMASKEQQIQRDDPGASPQSSSQPDHGRLSPPEAPDRPTISTASE
TSVYVTWI PRGNGGFPIQSFRVEYKKLKVGDWILATS AIPPSRLSVEITGLEKGTSYKFRV
RALNMLGESEPSAPS RPYVVSGYSGR VYERPVAGPYITFTDAVNETT IMLKWMYIPASNNNT
PIHGFYI YYRPT DSDNDSDYKKDMVEGDKYWH SISHLQPETSYDIKMQCFNEGGEFSNVM
ICETKARKSSGQPGR LPPPTLAPPQPLPETIERPVGTGAMVARSSDLPYLIVGVVLGSIVL
IIVTFIPFCLWRAWSKQKHTDLGFPR SALPPSCP YTMVPLGGLPGHQASGQPYLSGISGRA
CANGIHMNRGCP SAAVGYPGMKPQQHCPGELQQQSDTSSLLRQTHLGNGYDPQSHQITRGPK
SSPDEGSFLYTL PDDSTHQLLQPHDCCQ RQEOPA AVGQSGVRRAPDSPVLEAVWDPPFHSG
PPCCLGLVPVEEV DSDSCQVSGGDWCPQHPVGA YVGQEPGMQLSPGPLVRVS FETPPLTI

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 16-30 (type II), 854-879



37/249

FIGURE 37

CGGGAGGCTGGTCGTATGATCCGGACCCATTGTCGGCCTCTGCCCATGCCTGCTCCTC
CCAGGCTCCCGGCCGACCCCCGCGAACATGCAGCCCACGGGCCGAGGGTTCCCGCGC
GCTCAGCCGGCGGTATCTGCGCGTCTGCTGCTCCTGCTACTGCTGCTGCTGCGGCAGC
CCGTAACCCGCGGGAGACCACGCCGGCGCCCCAGAGCCCTCTCCACGCTGGCTCCCC
AGCCTCTTCAACCACGCCGGGTGTCCCCAGGCCCTCACTACCCAGGCCACTACGCCAGG
CACCCCCAAAACCTGGACCTTCGGGGTCGCGCGCAGGCCCTGATGCGGAGTTCCACTCG
TGGACGGCCACAATGACCTGCCAGGTCTGAGACAGCGTTACAAGAATGTGCTTCAGGAT
GTTAACCTGCGAAATTTCAGCCATGGTCAGACCAGCCTGGACAGGCTTAGAGACGGCCTCGT
GGGTGCCAGTTCTGGTCAGCCTCCGTCTCATGCCAGTCCCAGGACCAGACTGCCGTGCGCC
TCGCCCTGGAGCAGATTGACCTCATTCACCGCATGTGTGCCCTACTCTGAACCTCGAGCTT
GTGACCTCAGCTGAAGGTCTGAACAGCTCTCAAAAGCTGCCCTGCCTCATTGGCGTNAGGG
TGGTCACTCACTGGACAGCAGCCTCTGTGCTGCCAGTTCTATGTGCTGGGGTGCGCT
ACCTGACACTTACCTTCACCTGCAGTACACCATGGCAGAGAGTTCCACCAAGTTCAGACAC
CACATGTACACCAACGTCA CGGGATTGACAAGCTTGGTAGAAAGTAGTAGAGGGAGTTGAA
CCGCCTGGCATGATGATAGATTGCTCTATGCATCGGACACCTTGATAAGAAGGGCCTGG
AAGTGTCTCAGGCTCCTGTGATCTTCTCCACTCAGCTGCCAGAGCTGTGTGACAATTG
TTGAATGTTCCCGATGATATCCTGCAGCTCTGAAGAACGGTGGCATCGTGTGACACT
GTCCATGGGGTGCTGCAGTGCAACCTGCTGCTAACGTGTCCACTGTGGCAGATCACTTG
ACCACATCAGGGCAGTCATTGGATCTGAGTTCATCGGGATTGGTAGAAATTATGACGGACT
GGCCGGTCCCTCAGGGCTGGAGGATGTGTCACATACCCAGTCCTGATAGAGGGAGTTGCT
GAGTCGTASCTGGAGCGAGGAAGAGCTTCAAGGTGTCCTCGTGGAAACCTGCTGCCGGTCT
TCAGACAAGTGGAAAAGGTGAGAGAGGAGAGCAGGGCGCAGAGCCCCGTGGAGGCTGAGTT
CCATATGGCAACTGAGCACATCCTGCCACTCCCACCTCGTGCCTCAGAATGGACACCAGGC
TACTCATCTGGAGGTGACCAAGCAGCCAACCAATGGGTCCCTGGAGGTCTCAAATGCCT
CCCCATACCTTGTCCAGGCCTTGTGGCTGCCACCATCCAACCTCACCCAGTGGCTC
TGTGAACAGTCGGTCCCCGAGAGGTCACTGTGGCAAAGCCTCACAAAGCCCCCTCTCCT
AGTTCATTCACAAGCATATGCTGAGAATAAACATGTTACACATGGAAAA



38/249

FIGURE 38

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59817
><subunit 1 of 1, 487 aa, 1 stop, 2 unknown
><MW: 53569.32, pI: 7.68, NX(S/T): 5
MQPTGREGSRALSRYYLRRLLLLLLLLLRLQPVTRAETTPGAPRALSTLGSPSLFTTPGVPS
ALTTPGLTTPGTPKTLDLRGRAQALMRSFPLVDGHNDLPQVLRQRYKNVLQDVNLRNFSHGQ
TSLDRLRDGLVGAQFWSASVSCQSQDQTAVRLALEQIDLIHRMCASYSELELVTSAEGLNSS
QKLACLIGVXGGHSLDSSLVLSFYVLGVRYLTFTCSTPWAESSTKFRHHMYTNVSGLT
SFGEKVVEELNRLLGMMIDLSSYASDTLIRRVLEVSQAPVIFSHSAARAVCDNLLNVPDDILQL
LKNGGIVMVTLMSGVLQCNLLANVSTVADHFDHIRAVIGSEFIGIGGNYDGTGRFPQGLEDV
STYPVLLIEELLSRXWSEEELQGVLRGNLLRVFRQVEKREESRAQSPVEAEFPYQQLSTSCH
SHLVPQNGHQATHLEVTKOPTNRVPWRSSNASPYLVPGLVAAATIPTFTQWLC

Important features of the protein:

Signal peptide:

amino acids 1-36

Transmembrane domain:

amino acids 313-331

N-glycosylation sites.

amino acids 119-122, 184-187, 243-246 and 333-336

N-myristoylation sites.

amino acids 41-46, 59-64, 73-78, 133-138, 182-187, 194-199, 324-329, 354-359, 357-362, 394-399, 427-432 and 472-477.

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 136-146



FIGURE 39

TGCTAGGCTCTGCCACAATGCACCCGAGAGCAGGAGCTGAAAGCCTCTAACACCCACAGA
TCCCTCTATGACTGCAATGTGAGGTGTCCGGCTTGCTGGCCAGCAAGCCTGATAAGC**ATG**
AAGCTCTTATCTTGGTGGCTGTGGCGGGTGTGCTGGTCCCCCAGCTGAAGCCAACAA
GAGTTCTGAAGATATCCGGTGCAAATGCATCTGTCCACCTTATAGAAACATCAGTGGGCACA
TTTACAACCAGAATGTATCCCAGAAGGACTGCAACTGCCTGCACGTGGTGGAGCCCATGCCA
GTGCCTGGCCATGACGTGGAGGCCTACTGCCTGCTGTGCGAGTGCAGGTACGAGGAGCGCAG
CACCACCAACATCAAGGTACATTGTCATCTACCTGTCCGTGGTGGGTGCCCTGTTGCTCT
ACATGGCCTTCCTGATGCTGGTGGACCCTCTGATCCGAAAGCCGGATGCATAACTGAGCAA
CTGCACAATGAGGAGGAGAATGAGGATGCTCGCTCTATGGCAGCAGCTGCTGCATCCCTCGG
GGGACCCCGAGCAAACACAGTCCTGGAGCGTGTGGAAGGTGCCAGCAGCGGTGGAAGCTGC
AGGTGCAGGAGCAGCGGAAGACAGTCTCGATCGGCACAAGATGCTCAGC**TAG**ATGGGCTGG
TGTGGTTGGGTCAAGGCCAACACCATGGCTGCCAGCTCCAGGCTGGACAAAGCAGGGGG
CTACTTCTCCCTCCCTCGGTTCCAGTCTCCCTTAAAAGCCTGTGGCATTTTCCCTCCTT
CTCCCTAACTTTAGAAATGTTGTACTGGCTATTGATTAGGGAAGAGGGATGTGGTCTCT
GATCTCTGTTGTCCTGGTCTTGGGTTGAAGGGAGGGGAAGGCAGGCCAGAAGGGA
ATGGAGACATTGAGGCGGCCTCAGGAGTGGATGCGATCTGTCCTCCTGGCTCCACTCTG
CCGCCTTCCAGCTCTGAGTCTGGGAATGTTGTTACCTTGGAAAGATAAAAGCTGGGTCTTCA
GGAACTCAGTGTCTGGAGGAAAGCATGGCCAGCATTGAGCATGTGTTCTGGCTGCAGTG
GTTCTTATCACCAACCTCCCTCCAGCCCCGGCCTCAGCCCCAGCCCCAGCTCCAGCCCTG
AGGACAGCTCTGATGGGAGAGCTGGGCCCCCTGAGCCCAGTGGTCTTCAGGGTGCAGTGG
AGCTGGTGGTGCCTGTCCTGCACTTCTCGCACTGGGCATGGAGTGCCTGCAGTGCATACT
CTGCTGCCGGTCCCTCACCTGCACTTGAGGGGTCTGGCAGTCCCTCTCCCCAGTGTG
CACAGTCAGTGCAGGCCAGACGGTCGGTTGGAACATGAGACTCGAGGCTGAGCGTGGATCTGAA
CACCAACAGCCCCGTACTTGGGTTGCCTCTGTCCCTGAACCTCGTTGTAACAGTGCATGG
GAGAAAATTTGTCCTCTGTCTTAGAGTTGTGTAAATCAAGGAAGCCATCATTAAATTG
TTTATTTCTCTCA



40/249

FIGURE 40

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60278
<subunit 1 of 1, 183 aa, 1 stop
<MW: 20574, pI: 6.60, NX(S/T): 3
MKLLSLVAVVGCLLVPPEAEANKSSEDIRCKCICPPYRNISGHLYNQNVSQKDCNCLHVVEPM
PVPGHDVEAYCLLCECRYERSTTIKVIIIVIYLSVGALLLYMAFLMLVDPLIRKPDAYTE
QLHNEEENEDARSMAAAASLGGPRANTVLERVEGAQQRWKLQVQEQRKTVFDRHKMLS
```

Important features:

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 90-112

N-glycosylation sites.

amino acids 21-24, 38-41 and 47-50



41/249

FIGURE 41

AGCGGGTCTCGCTGGGTTCCGTAATTCGCTGAGCGTGAGACTGAGTCATAGGTCTGGTCCCCGA
ACCGAGAAGGGTGAGGAACACAATCTGCAAGCCCCCGCACCAGTGAAGGGCCCCGTGTTGGGTCTCCC
TCCCTTGCACTCCCACCCCTCCGGGCTTGCCTCTCTGGGACCCCCTGCCGGAGATGGCCGCGTTGATG
CGGAGCAAGGATTGCTCTGCCGCTCCTACTGGCCGCGGTGCTGATGGTGGAGAGCTCACAGATCGGAGT
TCGGGGCAAACCTCAACTCCATCAAGTCTCTGGGCGGGAGACGCGTGGTCAAGGCCAACATGATCTGCG
GGCATGTACCAAGGACTGGCATTGGCGGAGTAAGAAGGGCAAAACCTGGGCAAGGCCAACCTGTAGCAGT
GATAAGGAGTGTGAAGTTGGAGGTATTGCCACAGTCCCCACCAAGGATCATGGCCTGCATGGTGTGCGAGA
AAAAAGAAGCGCTGCCACCGAGATGGCATGTGCTGCCAGTACCGCTGCAATAATGGCATCTGTATCCCAGTT
ACTGAAAGCATCTAACCCCTCACATCCGGCTGGATGGTACTCGGCACAGAGATCGAAACCACGGTATTAC
TCAAACCATGACTGGGATGGCAGAACATCTAGGAAGACCACACACTAAGATGTCACATATAAAAGGGCATGAAGGA
GACCCCTGCCCTACGATCATCAGACTGCATTGAAGGGTTTGTGCTGCTGTCATTCGACCAAAATCTGAAA
CCAGTGCCTCATCAGGGGAAAGTCTGTACCAAACACGCAAGAAGGGTCTCATGGGCTGGAAATTTCAGCGT
TGCAGTGTGCGAAGGGCCTGCTGCAAAGTATGAAAGATGCACCTACTCCTCCAAAGCCAGACTCCATGTG
TGTCAAGAAAATTTGATCACCATTGAGGAACATCATCAATTGAGACTGTGAAGTTGTATTTAATGCAATTAG
CATGGTGGAAAATAAGGTTAGATGCAGAACATGGCTAAAATAAGAACCTGATAAGAATATAGATGATCACAA
AAAGGGAGAAAGAAACATGAACATGAATAGATTAGAATGGGTGACAAATGAGTGCAGTCAGGCGACTGTTCCATTATG
CAACTTGTCTATGTAATAATGACACATTGAGGAAATTGCTATTAAAGAGAACAGCACACAGTGGAAATT
ACTGATGAGTAGCATGTGACTTCCAAGAGTTAGGTTGTGCTGGAGGAGAGGTTCTCAGATTGCTGATTGC
TTATCAAATAACCTACATGCCAGATTCTATTCAACGTTAGAGTTAACAAAATCTCTAGAATAACTTGTAA
TACAATAGGGTCTAAAAATAAGGCTAAACAAGAACATGGAGCATTGTTAATTACAACAGAAAAT
TACCTTTGATTTGTAACACTACTCTGCTGTTCAATCAAGACTTGGTAGATAAGAAAAAAATCAGTCATA
TTCCAAATAATTGCAAAATAATGGCAGTTGTTAGGAAGGCCTTTAGGAAGACAAATAACAAACAG
CCACAAATACTTTTTCAAAATTAGTTACCTGTAATTAAAGAACATGATACAAGACAAAACAGTCC
TTCAGATTCTACGGAATGACAGTATATCTCTTTATCCTATGTGATTCTGCTGATGCAATTATTTCCA
AACTATACCCATAATTGTAACAGTAAACACTTACACAGAGCAGAATTTCACAGATGGCAAAAAAATTAAA
GATGTCCAATATATGAGGAAAGAGCTAACAGAGAGATCATTATTCTAAAGATTGGCATAACCTATA
GATAGAATTAGATTGGTAAATACTGATTCATACATACTCTGTTGTAATTAGAGACTTAAGCTGGATCTGACTG
CACTGGAGTAAGCAAGAAAATTGGGAAAACCTTTCTGTTGCTCAGGTTTGGCAACACATAGATCATATGCTG
AGGCACAAGTTGGCTTCACTTGAACAGGAGGAGTCACAGCTAAATGAATATCTGCATGGATTGCTAT
CATAATTACTATGAGATGAAATTGAGCTTCAATTGAGGTTCTGTTGAGGTTCTGCTGACTATCCTCAAATT
TGCAGTGTGAGATCTCAAATACTCAATTGAGGTTCTGAGGTTCAACAAATGTAACGAGACTGAG
TTTCATTGCCCTCTATAAGCTCTGACTAGCCAATGGCATCATCCAATTCTCCAAACCTCTGCAGCATCTG
CTTATTGCAAAAGGCTAGTTCGGTTCTGCAGCCATTGCGGTTAAAAAATATAAGTAGGATAACTGTAAA
ACCTGCATATTGTAATCTATAGACACCACAGTTCTAAATTCTTGAACCAACTTACTACTTTAAACTT
AACTCAGTTCTAAATACTTGTCTGGAGCACAAAACAATAAGGTTATCTTATAGTCGTGACTTTAAACTTTG
TAGACCACAATTCACTTTTAGTTCTTTACTTAAATCCCCTGCACTGCAAGTCACAAATTAAAGTTCTCCAGTAG
AGATTGAGTTGAGCCTGTATATCTATTAAACATTCAACTTCCCACATATATTACTAAGATGATTAAGACTTA
CATTTCTGCACAGGTCTGCAAAACAAAATTATAAACTAGTCCATCCAAGAACCAAAGTTGTATAAACAGGT
TGCTATAAGCTGTGAAATGGAACATTCAATCAAACATTCTATATAACAAATTATTATTTACAAT
TTGGTTCTGCAATTATTCTTATGTCCACCCCTTTAAAAATTATTGAGTAATTATTACAGGAAATG
TTAATGAGATGTATTCTTCTTATAGAGATATTCTTACAGAAAGCTTGTAGCAGAATATATTGCA
TTTGTAAATTAGGAAAAATGTATAAAAGATAAAACTTATTAATTTCTCTAAACTGAAAAAAA
AAAAAAAAAAAAAAA



SEARCHED SERIALIZED INDEXED

42/249

FIGURE 42

MAALMRSKDSSCCLLLAAVLMVESSQIGSSRAKLSNIKSSLGGETPGQAANRSAGMYQGLA
FGGSKKGKNLGQAYPCSSDKECEVGRYCHSPHQGSSACMVCRKKRCHRDGMCCPSTRCNN
GICIPVTESILTPHIPALDGTRHRDRNHGHYSNHDLGWQNLGRPHTKMSHIKGHEGDPCRLS
SDCIEGFCCARHFWTKICKPVLHQGEVCTKQRKKGSHGLEIFQRCDCAKGLSCKVWKDATYS
SKARLHVQCQKI

Signal peptide:

amino acids 1-25



FIGURE 43

TCTCAATCTGCTGACCTCGTGATCCGCCTGACCTGTAATCCACCTACCTGGCCTCCAAA
GTGTTGGGATTACAGGCGTGAGCCACCGCGCCGGCCAACATCACGTTTAAAAATTGATT
TCTTCAAATTATGGCAAATATTCCTCCCTTAACCTTATGTAGAATGAGGAAGGA
TAGCTGCATTATTTAGTCAGTTCATGCATAGTAATATTCATGTAGTATTTCTAAG
TTATATTTAGTAATTCATATGTTAGATTAGGTTAACATACTTGTGAAAATACTG
ATGTGTTTAAAGCCTGGCAGAAATTCTGTATTGTTGAGGATTGTTCTTATCCCCCT
TTAAAGTCATCCGTCCTGGCTCAGGATTGGAGAGCTGCACCACCAAAATGGCAAACA
TCACCAGCTCCCAGATTTGGACCAGTGAAAGCTCGAGTTGGCCAGTTACCAACC
CCAAGTACACAGCAGAATAGTACAAGTCACCCCTACAACACTACTTCTGGACCTCAAGCC
CCCAACATCCCAGTCCTCAGTCATCTGACTCAAATCTAACCTGAGCCATCCC
CAGTTCTAGCCAGTTGAGCCAGCGACAACAGCACCAGAGCCAGGCAGTCAGTGTCTCCT
CCTGGTTGGAGTCCTTCTCCAGGCAAAACTTCGAGAATCAACACCTGGAGACAGTCC
CTCCACTGTGAACAAGCTTGCAGCTCCAGCAGCACCATTGAAAATATCTGTGTCTG
TCCACCAGCCACAGCCAAACACATCAAACATTGCTAACGGCGGATACCCCCAGCTCTAAG
ATCCCAGCTCTGCAGTGGAAATGCCGGTCAGCAGATGTACAGGATTAAATGTGCAGTT
TGGGGCTCTGGAATTGGGTCAAGAACCTCTCTGAATTGGATCAGCTCAAAGCAGTG
AAAATAGTAATCAGATTCCATCAGCTGTATTGAAGTCTTAAGTGAGCCTTGAATACA
TCTTATCAATGACCACTGCAGTACAGAACTCCACATATAACACTCCGTATTACCTCCTG
CAGTCTGACAAGCTCATCACTGAATTCTGCTAGTCCAGTAGCAATGTCTCCTTATGACC
AGAGTTCTGTGCATAACAGGATCCATACAAAGCCCTGTGAGTCATCAGAGTCAGCTCCA
GGAACCATCATGAATGGACATGGTGGTGGTCGAAGTCAGCAGACACTAGACAGTAAGTATAG
CAGCAAGCTACTCTGTATGGCTGGTGCCTAATGGCTCATTGCTTGGGAAAGAGGAGGT
TGTGGAAAACACCAGTTGGTCAATGGCTCATTGCTTGGGAAAGCAGCCCTTTGCTTTTGT
TTTGGACCAGGTGTTGGCTGTGGTATTAGAAATGTCTTAACCACAGCAAGAAGGGAGGT
GGTGGTCTCATATTCTGCCCTAATCAGACTGCACCACAGTCAGCAGCATACAGTATGCAT
TTAAAGATGCTTGGCCAGGCAGGGTGGCTGATGCCATAATCCAGTGCTTGGGGCC
AAGGCAGGCAGATTGCCAAGCTCAGGAGTTGAGACCACCCCTGGCAACATGGTAAACTC
TGTCTACTAAAATCAGAAAAACTAGCCGGGTGTGGTGGCGCGCGTGCCTGTAATCCCAG
CTACTTGGGAGGCTGAGGCACAAGAATCGCTTGAGCCAGCTGGCTACAAAGTGAGACTCC
GTCTGAAAAGA



44/249

FIGURE 44

MCFKALGRNSVLLRICSFIPLLKSSVLGSGFHELAPPKMANITSSQILDQLKAPSLGQFTTT
PSTQQNSTSHPTTTSWDLKPPTSQSSVLSHLDFKSQPEPSPVLSQLSQRQQHQSQAVTVPP
PGLESFPSQAKLRESTPGDSPSTVNKLLQLPSTTIENISVSVHQPQPKHIKLAKRRIPPASK
IPASAVEMPGSADVTGLNVQFGALEFGSEPSLSEFGSAPSSENSNQIPISLYSKSLSEPLNT
SLSMTSAVQNSTYTTSVITSCSLTSSLNSASPVAMSSSYDQSSVHNRIPYQSPVSSSESAP
GTIMNGHGGGRSQQTLD SKYSSKLLSWLVPTKQRKRIAHV MWKTPVGQWLIR

Signal peptide:

amino acids 1-24

FIGURE 45

GCCGAGTGGACAAAGCCTGGGCTGGCGGGGCCATGGCGCTGCCATCCGAATCCTGCT
 TTGGAAACTTGTGTTCTGCAGAGCTCTGCTGTTCTCCTGCACTCAGCGGTGGAGGAGACGG
 ACGCGGGCTGTACACCTGCAACCTGCACCACACTACTGCCACCTCTACGAGAGCCTGCC
 GTCCGCCTGGAGGTACCGACGGCCCCCGGCCACCCCGCCTACTGGGACGGCGAGAAGGA
 GGTGCTGGCGGTGGCGCGCGCACCCCGCCTCTGACCTGCGTAACCGCGGGCACGTGT
 GGACCGACCGGACGTGGAGGAGGCTAACAGGTGGTCACGGGACCGGCAGCCGCCGGG
 GTCCCGCACGACCGCGCGGACCGCCTGCTGGACCTCTACGCGTCGGCGAGCGCCGCC
 CGGGCCCTTTCTGCGCACCGCGTGGCTGTGGCGCGATGCCTTGAGCGCGGTGACT
 TCTCACTGCGTATCGAGCCGCTGGAGGTGCCGACGAGGGCACCTACTCCTGCCACCTGCAC
 CACCATTACTGTGGCCTGCACGAACGCCGCTTCCACCTGACGGTCGCCAACCCCACGC
 GGAGCCGCCCCCCCAGGGCTCTCCGGCAACGGCTCCAGCCACAGCGGCCAGGCCCAG
 ACCCCACACTGGCGCGGCCAACAGTCATCAATGTCATCGTCCCCAGAGAGCCGAGCCCAC
 TTCTTCAGCAGCTGGCTACGTGCTGGCACGCTGCTCTCATCCTGCTACTGGTCAC
 TGTCCCTGGCCGCCGCAGGCGCCGGAGGCTACGAATACTGGACCAAGAGTCGGAA
 AGTCAAAGGGAAAGGATGTTAACTGGCGAGTTGCTGTGGCTGCAGGGGACAGATGCTT
 TACAGGAGTGAGGACATCCAGCTAGATTACAAAAAACATCCTGAAGGAGAGGGCGGAGCT
 GGCCCACAGCCCCCTGCCAGTACATCGACCTAGACAAAGGGTCCGAAGGGAGAAGACT
GCAAATAGGGAGGCCCTGGCTCCCTGGCTGGCCAGCAGCTGCACCTCTCCTGTGCTC
 CTCGGGCATCTCCTGATGCTCCGGGCTCACCCCCCTCCAGCGGCTGGTCCGCTTCC
 GGAATTGGCCTGGCGTATGCAGAGGCCCTCCACACCCCTCCCCAGGGCTTGGTGG
 AGCATAGCCCCACCCCTGCCCTTGTACGGGTGGCCCTGCCACCCCTGGCACAA
 AAAATCCCACGTGATGCCCATCATGCCCTCAGACCCCTCTGGCTCTGCCGCTGGGGCCTG
 AAGACATTCCCTGGAGGACACTCCCATCAGAACCTGGCAGCCCCAAACTGGGTGAGCCTCA
 GGGCAGGAGTCCCACTCCTCCAGGGCTCTGCTCGTCCGGGCTGGAGATGTTCTGGAGGA
 GGACACTCCCACAGAACCTGGCAGCCTGAAAGTTGGGTGAGCCTCGGCAGGAGTCCCACT
 CCTCCTGGGTGCTGCCACCAAGAGCTCCCCACCTGTACCAACCATGTGGACTCCAG
 GCACCATCTGTTCTCCCCAGGGACCTGCTGACTTGAATGCCAGCCCTGCTCCTCTGTGTTG
 CTTGGGCCACCTGGGCTGCACCCCTGCCCTTCTGCCCTACCCCTACCCCTAGCCTG
 CTCTCAGGCCACCTGATAGTCAGGGCTCCCTGTGACTTCTGACCCCTGACACCCCTCC
 GGACTCTGCCTGGCTGGAGTCTAGGGCTGGGCTACATTGGCTTGTACTGGCTGAGGA
 CAGGGGAGGGAGTGAAGTGGTTGGGTGGCCTGTGTTGCCACTCTCAGCACCCACATT
 GCATCTGCTGGTGGACCTGCCACCATCACAATAAGTCCCCATCTGATTTAAAAAAAA
 AAAAAA



46/249

FIGURE 46

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60618
<subunit 1 of 1, 341 aa, 1 stop
<MW: 38070, pi: 6.88, NX(S/T): 1
MALPSRILLWKLVLLQSSAVLLHSAVEETDAGLYTCNLHHHYCHLYESLAVRLEVTDGPPAT
PAYWDGEKEVLAVARGAPALLTCVNRGHVWTDRHVEEAQQVWHWRDQPPGVPHDRADRLLDL
YASGERRAYGPLFLRDRVAVGADAFERGDFSLRIEPLEVADEGTYSCHLHHHYCGLHERRVF
HLTVAEPAEPPPGRSPGNNGSSHSGAPGPDP TLARGHNVINVIVPESRAHFFQQLGYVLA
LLFILLLVTVLLAARRRRGGYEYSQKSGKSKGDVNLAFAVAAGDQMLYRSEDIQLDYKN
NILKERAELAHSPLPAKYIDL DKGFRKENCK
```

Important features:

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 237-262

N-glycosylation site.

amino acids 205-208

Cell attachment sequence.

amino acids 151-154

Coproporphyrinogen III oxidase proteins.

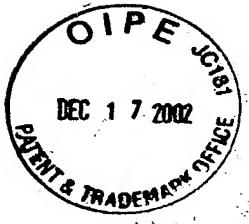
amino acids 115-140



47/249

FIGURE 47

CGCCGGAGGCAGCGCGGTGGCGCAGCGCGAC**ATG**GCCGTTGTCAGAGGACGACTTT
CAGCACAGTCAAACCTCACCGAACACAAGCAGCAGTCTCCGAGCTGACCAGGAGGC
ACTGCTTGAGAAGCTGCTGGACCGCCCCCTGGCCTGAGAGGCCCAGGACCGCTTCT
GTGGCACATACATCATCTTCTCAGCCTGGCATTGGCAGTCACTGCCATGGAACCTCTT
ATCACTGCCAAGGAGTACTGGATGTTCAAACCTCGCAACTCCTCCAGCCCAGCCACC
GGACCCCTGAGGGCTCAGACATCCTGAACACTTTGAGAGCTACCTTGGCGTTGCCTCCACCG
TGCCCTCCATGCTGTGCCTGGCTGGCAACTCCTGCTGTCAACAGGGTTGCAGTCCACATC
CGTGTCCCTGGCCTCACTGACGGTCATCCTGCCATCTCATGGTATAACTGCACTGGTGAA
GGTGGACACTTCCCTCTGGACCCGTGGTTTTTGCGGTCACCATTGCTGATGGTATGCC
TCAGCGGTGCCTCCACTGTCTTCAGCAGCAGCATCTACGGCATGACCGGCTCCTTCATG
AGGAACCTCCAAGCACTGATATCAGGAGGAGCCATGGGCGGACGGTCAGCGCCGTGGCTC
ATTGGTGGACTTGGCTGCATCCAGTGATGTGAGGAACAGCGCCCTGGCCTTCTCCTGACGG
CCACCATCTCCTCGTGCATGGACTCTACCTGCTGTCCAGGCTGGAGTATGCC
AGGTACTACATGAGGCCTGTTCTTGGCCATGTGTTCTGGTGAAGAGGAGCTCCCCA
GGACTCCCTCAGTGCCTGGCTCCAGATTGATTCCCACACACCCCCCTCTCC
GCCCATCTGAAGAACGGCCAGCCTGGCTCTGTGTCACCTACGTCTTCTCATCACC
AGCCTCATCTACCCGCCGTCTGCACCAACATCGAGTCCCTCAACAAGGGCTGGGCTCACT
GTGGACCACCAAGTTTCATCCCCCTCACTACCTCCCTGTACAACACTTGCTGACCTAT
GTGGCCGGCAGCTACCGCCTGGATCCAGGTGCCAGGGCCAACAGCAAGGCCTCCAGGG
TTCGTGCTCCTCCGGACCTGCCTCATCCCCCTCTCGTGTCTGTAACCTACAGCCCCGCT
CCACCTGAAGACTGTGGTCTTCCAGTCCGATGTGTACCCGACTCCTCAGCTCCGTGG
GGCTCAGCAACGGCTACCTCAGCACCCCTGGCCCTCCTCTACGGGCTAAGATTGTGCCAGG
GAGCTGGCTGAGGCCACGGGAGTGGTGTGCTTTATGTGTGCTGGCTTAACACTGGG
CTCAGCCTGCTCACCCCTCTGGTGCACCTCATC**TAG**AAGGGAGGACACAAGGACATTGGT
CTTCAGAGCCTTGAAGATGAGAAGAGACTGCAGGAGGGCTGGGGCCATGGAGGAAGGCC
TAAAGTTCACTTGGGGACAGAGAGCAGAGCACACTCGGGCCTCATCCCTCCAAAGATGCCA
GTGAGCCACGTCCATGCCATTCCGTGCAAGGCAGATATTCCAGTCATATTACAGAACACT
CCTGAGACAGTTGAAGAAGAAATAGCACAAATCAGGGTACTCCCTCACAGCTGATGGTTA
ACATTCCACCTTCTTCTAGCCCTCAAAGATGCTGCCAGTGTGCCCCTAGAGTTATTACA
AAGCCAGTGCACAAACCCAGCCATGGCTTTGCAACCTCCAGCTGCGCTATTCCAGCT
GACAGCGAGATGCAAGCAAATGCTCAGCTCCTTACCCCTGAAGGGCTCCCTGGAATGGA
AGTCCCCTGGCATGGTCAGTCCCTCAGGCCAACAGACTCAAGTGTGCACAGACCCCTGTGTTCT
GGGGGTGAACAACTGCCACTAACAGACTGGAAAACCCAGAAAGATGGGCCTCCATGAAT
GCTTCATTCCAGAGGGACAGAGGGCTCCCTGTGCAAGGGATCAAGCATGTCTGGCCTGGG
TTTCAAAAAAAGAGGGATCCTCATGACCTGGTGTCTATGGCCTGGTCAAGATGAGGGTC
TTTCAGTGTCCCTGTTACAACATGTCAAAGCCATTGGTTCAAGGGCGTAATAAAACTTGC
GTATTCAAAAA



SEARCHED SERIALIZED FILED DECEMBER 17 2002

48/249

FIGURE 48

MAVVSEDDFQHSSNSTYGTSSSLRADQEALLEKLLDRPPPGLQRPEDRFCGTYIIFPSLGI
GSLLPWNNFFITAKEYWMFKLRNSSSPATGEDPEGSDILNYFESYLA VASTVPSMLCLVANFL
LVNRVAVHIRVLASLTVILAIFMVITALVKVDTSSWTRGFFAVTIVCMVILSGASTVFSSSI
YGMTGSFPMRNSQALISGGAMGGTVSAVASLVDLAASSDVRNSALAFFLTATIFLVLCMGLY
LLLSRLEYARYYMRPVLAHVFSGEEELPQDSLSAPSVASRFIDSHTPPLRPILKKTASLG
CVTYVFFITSLIYPAVCTNIESLNKGSGSLWTTKFFIPLTTFLYNFADLCGRQLTAWIQVP
GPNSKALPGFVLLRTCLIPLFVLCNYQPRVHLKTVVFQSDVYPALLSLLGLSNGYLSTLAL
LYGPKIVPRELAEATGVVMSFYVCLGLTLGSACSTLLVHLI

Transmembrane domain:

amino acids 50-74 (type II), 105-127, 135-153, 163-183, 228-252,
305-330, 448-472



49/249

FIGURE 49

GACAGTGGAGGGCAGTGGAGAGGACCGCGCTGTCCTGCTGTACCAAGAGCTGGAGACACCA
TCTCCCACCGAGAGTCATGGCCCCATTGGCCCTGCACCTCCTCGTCCTCGTCCCCATCCTCC
TCAGCCTGGTGGCCTCCCAGGACTGGAAGGCTGAACGCCAGCCAAGACCCCTCGAGAAATGC
ATGCAGGATCCTGACTATGAGCAGCTGCTCAAGGTGGTACCTGGGGCTCAATCGGACCC
GAAGCCCCAGAGGGTGATTGTGGTTGGCGCTGGTGTGGCCGGCTGGTGGCCGCAAGGTGC
TCAGCGATGCTGGACACAAGGTACCACATCCTGGAGGCAGATAACAGGATCGGGGCCGCATC
TTCACCTACCGGGACCAGAACACGGGCTGGATTGGGAGCTGGGAGCCATGCGCATGCCAG
CTCTCACAGGATCCTCCACAAGCTCTGCCAGGGCTGGGCTAACCTGACCAAGTTACCC
AGTACGACAAGAACACGTGGACGGAGGTGCACGAAGTGAAGCTGCGCAACTATGTGGTGGAG
AAGGTGCCCGAGAACAGCTGGCTACGCCCTGCGTCCCCAGGAAAAGGGCCACTGCCCGAAGA
CATCTACCAGATGGCTCTCAACCAGGCCCTCAAAGACCTCAAGGCAGTGGCTGCAGAAAGG
CGATGAAGAACAGTTGAAAGGCACACGCTCTTGGAAATATCTTCTCGGGAGGGAACCTGAGC
CGGCCGGCCGTGCAGCTCTGGAGACGTGATGTCCGAGGATGGCTTCTTCTATCTCAGCTT
CGCCGAGGCCCTCGGGCCCACAGCTGCCAGCGACAGACTCCAGTACAGCCGCATCGTGG
GTGGCTGGACCTGCTGCCCGCGCTGCTGAGCTCGCTGCCGGCTTGTGCTGTTGAAC
GCGCCCGTGGTGGCGATGACCCAGGGACCGCACGATGTGCACGTGCAGATCGAGACCTCTCC
CCCGGCCGGAATCTGAAGGTGCTGAAGGCCGACGTGGTGTGCTGACGGCGAGCGGACCGG
CGGTGAAGCGCATCACCTCTGCCGCCGCTGCCCGCACATGCAGGAGGCAGTGCAGGAGG
CTGCACTACGTGCCGCCACCAAGGTGTTCTAACGCTTCCGCAGGCCCTCTGGCGCGAGGA
GCACATTGAAGGCCGCACTCAAACACCGATGCCCGTCGCCATGATTTCTACCGCCGC
CGCGCAGGGCGCGCTGCTGCTGGCCTCGTACACGTGGTGGACGCCGGCAGCGTTCGCC
GGCTTGAGCCGGGAAGAGGCAGTGGCTTGGCCTCGACGACGTGGCGCATTGCACGGGCC
TGTCGTGCCAGCTCTGGACGGCACCGCGTCGTCAAGCGTTGGCGAGGACAGCACA
GCCAGGGTGGCTTGTGGTACAGCCGCCGCTCTGGCAAACCGAAAAGGATGACTGGACG
GTCCCTTATGGCCGCATCTACTTGCCTGGAGCACACCGCCTACCCGCACGGCTGGTGG
GACGGCGGTCAAGTCGGCGCTGCCGCATCAAGATCAACAGCCGGAAAGGGCCTGCAT
CGGACACGGCCAGCCCCGAGGGGCACGCATCTGACATGGAGGGCAGGGCATGTGCATGG
GTGGCCAGCAGCCCTCGCATGACCTGGCAAAGGAAGAAGGCAGCCACCCCTCCAGTCCAAGG
CCAGTTATCTCTCCAAAACACGACCCACACGGAGGACCTCGCATTAAAGTATTTCGGAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA



SEARCHED SERIALIZED INDEXED
DEPT OF COMMERCE

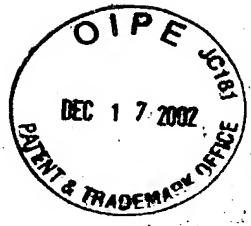
50/249

FIGURE 50

MAPLALHLLVLVPILLSLVASQDWKAERSQDPFEKCMQDPDYEQLLKVVWGLNRTLKPQRV
IVVGAGVAGLVAAKVLSDAHKVTILEADNRIGGIFTYRDQNTGWIGELGAMRMPSSHRL
HKLCQGLGLNLTKFTQYDKNTWTEVHEVKLRNYVVEKPEKLGYALRPQEKGHSPEDIYQMA
LNQALKDLKALGCRKAMKKFERHTILLEYLLGEGNLSRAVQLLGDVMSEDGFFYLSFAEALR
AHSCLSDRQLQYSRIVGGWDLLPRALLSSLGVLNNAPVVAMTQGPHDVHVQIETSPPARNL
KVLKADVLLTASGPRAVKRITFSPPPLPRHMQEALRRLHYVPATKVFLSFRRPFWREEHIEGG
HSNTDRPSRMIFYPPPREGALLSASYTWSDAAAFAGLSREEARLALDDVAALHGPVVRQL
WDGTGVVKRWAEDQHSQGGFVVQPPALWQTEKDDWTVPYGRIVFAGEHTAYPHGWETAVKS
ALRAAIKINSRKGPASDTASPEGHASDMEGQGHVHGVAASSPSHDLAKEEGSHPPVQGQLSLQ
NTTHTRTS

Signal peptide:

amino acids 1-21



2025 RELEASE UNDER E.O. 14176

51/249

FIGURE 51

CTGACATGGCCTGACTCGGGACAGCTCAGAGCAGGGCAGAACTGGGGACACTCTGGGCCGGCCTTCTGCCTGC**CAT**
GGACGCTCTGAAGCCACCCGTCTCTGGAGGAACCACGAGCAGGGAGAAGGACAGGGACTCGTGTGGCAGGAA
GAACTCAGAGCAGGGAGCAGCCCCATTCACTAGAACGACTGAGAGATGCGGCCCCCTCGCAGGGCTGAATTCCCT
GCTGCTGTTCACAAAGATGCTTTATCTTAACCTTTGTTTCCCACCTCCGACCCGGCTTGATCTGACCTGAA
CCTGACATTGGAGCTGCCATCTTCTGTGGCTGATCACAGAACCTCAACCCGTCTACCTCTTGACCTGAA
CAATCAGTCTGTGGAGATTGAGGGAGGAGCACGGAAGGGGTTCCCAAGAGGACTCGCTGTCTGACAATGGCCCTGCTGG
CTTCTCAGATGCCAAGACTATGTATGAGGTTTCCAAAGAGGACTCGCTGTCTGACAATGGCCCTGCTGG
ATATAGAAAACCAACCAGCCCTACAGATGGCTATCTTACAAACAGGTGCTGATAGAGCAGAGTACCTGGGTC
CTGTCTCTTCATCAAAGTTATAAATCATCACCAGACCAGTTGTCGGCATCTTGCTCAGAATAGGCCAGAGTG
GATCATCTCGAATTGGCTGTTACAGTACTCTATGGTAGCTGTACCTCTGTATGACACCTTGGGACCAGAAC
CATCGTACATATTGTCACAAGGCTGATATGCCATGGTATGTGACACACCCAAAAGGCATTGGTGTGAT
AGGGATGTAGAGAAAGGCTTACCCGAGCCTGAAGGTGATCATCCTATGGACCCCTTGATGATGACCTGAA
GCAAAGAGGGAGAAGAGTGAATTGAGATCTTATCCTATATGATGCTGAGAACCTAGGCAAAGAGCACCTAG
AAAACCTGTGCCCTCTAGGCCAGAACGACCTGAGCGTCATCTGCTTCAACCAGTGGGACCACAGGTGACCCAAAAGG
AGCCATGATAACCCATCAAATATTGTTCAAAATGCTGCTGCCCTCTCAAATGTGTTGAGGACTGCTTATGAGCC
CACTCCTGATGATGTGGCCATATCCTACCTCCCTGGCTCATATGTTGAGGAGTTGACAGGCTGTTGTGA
CAGCTGTGGAGCCAGAGTTGGATTCTCCAAGGGGATATTGGTTGCTGCCATGACGACATGAAGACTTTGAAGG
CACATTGTTCCCGGGTGCCTCGACTCCTAACAGGATCTACGATAAGGTACAAATGAGGCCAGACACCCCT
GAAGAAGTTCTTGTGAAGCTGGCTGTTCCAGTAATTCAAAGAGCTTCAAAAGGGTATCATCAGGCATGATAG
TTCTGGGACAAGCTCATCTTGCAAAGATCCAGGACAGCCTGGCGGAAGGGTCTGTGAATTGTCAGTGGAGC
TGCCCCCATGTCCACTCAGTCATGACATTCTCCGGCAGCAATGGGATGTCAGGTGATGAAAGCTTATGGTCA
AACAGAATGCACAGGGCTGTACATTACATTACCTGGGACTGGACATCAGGTACGTTGGGTTGCCCTGGC
TTGCAATTACGTGAAGCTGGAAAGATGTGGCTGACATGAACACTTACAGTGAATAATGAAGGAGGGCTGCT
CAAGGGTACAAACGTGTTCAAAGGATACCTGAAGGACCCCTGAGAACAGACAGGAAGCCCTGGACAGTGTGGCTG
GCTTCACACAGGAGACATTGGTCGCTGGCTCCGAATGGAACCTGAAAGATCATGACCGTAAAAAGAACATT
CAAGCTGGCCAAGGAGAACATTGACACAGAGAACGAGATAGAAAATATCTACACAGGAGTCACCAAGTGTACA
AATTGGTACACGGGGAGAGCTTACGGTCATCCTAGTAGGAGTGGTGGTCTGACACAGATGTACTTCCCTC
ATTGCAAGCCAAGCTGGGGTGAAGGGCTCTTGAGGAACCTGTCACAAACAGGTGAAAGGAGCCATT
AGAAGACTTGCAGAAAATTGGGAAAGAAAGTGGCTTAAACATTGAAACAGGCTAAAGCCATTTCATCC
AGAGCCATTTCATTGAAAATTGGCTCTGACACCAACATTGAAAGCAAGCAGGAGGAGCTTCCAAATACT
TCGGACCCAAATTGACAGCCTGTATGAGCACATCCAGGAT**TAG**GATAAGGTACTTAAGTACCTGCCGCCACTG
TGCACGTGTGAGAAAATTGGATTAAAACTATTCTACATTGTTGCTTCCCTATTGTTTAACC
TGTTAAACTCTAAAGCCATAGCTTTGTTATATTGAGACATATAATGTGTAAGACTAGTCCCAAATAATCA
ATCCTGTCTTCCATCTCGATGTTGCTAATATTAAGGCTCAGGGCTACTTTATCAACATGCCGTCTCAA
GATCCCAGTTATGTTCTGTGTCCTTCCATGATTCCAACCTTAATACTATTAGTAACCACAAGTTCAAGGGT
CAAAGGGACCTCTGTGCCCTCTTCTTGATAAACATAACTGCCAACAGTCTATGCTTATTACA
TCTTCTACTGTTCAAACTAAGAGATTAAATTCTGAAAAACTGCTTACAAATTGATTTCTAGCCACTCCAC
AAACCACTAAAATTGTTAGTTAGCCTACTCATGTCAATCATATCTAGAGACAAATGTCCTCGATGCTTT
CTGCGTAAATTAAATTGTTAGTGAAGGGAAAAGTTGATCATACCAACATTCTAAACTCTCTAGTTAGATA
TCTGACTTGGGAGTAAAAATTGGGTCTATGACATACTGTCCAAAAGGAATGCTGTTCTAAAGCATTATT
CAGTAGGAACCTGGGGAGTAAATGTTCCCTACAGTTGCTGAGCTGGAAGCTGTTGGGGAGGAGTTGACA
GGTGGGCCAGTGAACCTTCCAGTAATGAAGCAAGCACTGAATAAAACCTCTGAACTGGGAACAAAGATCT
ACAGGCAAGCAAGATGCCACACAACAGGTTATTCTGTGAAGGAACCAACTGATCTCCCCACCCCTGGATT
AGAGTTCTGCTCTACCTTACCCACAGATAACACATGTTGTTCTACTTGAAATGTTAAAGTCTTAAAATAAC
TATTACAGATAAAAAA



SEARCHED, SERIALIZED, INDEXED, COPIED

52/249

FIGURE 52

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60775
<subunit 1 of 1, 739 aa, 1 stop
<MW: 82263, pI: 7.55, NX(S/T): 3
MDALKPPCLWRNHERGKKDRDSCGRKNSEPGSPHSLEALRDAAPSQGLNFLLLFTKMLFIFN
FLFSPLPTPALICILTFGAIFIWLWLTTRPQPVLPLLDLNNQSVGIEGGARKGVSQKNNDLTS
CCFSDAKTMYEVFQRGLAVSDNGPCLGYRKPNQPYRWLSYKQVSdraeYLGSCLLHKGYKSS
PDQFVGIFAQNRPEWIISELACYTYSMVAVPLYDTLGPEAIHVHNKADIAMVICDTPQKAL
VLIGNVEKGFTPSSLKVIIILMDPFDDDLKQRGEKSGIEILSLYDAENLGKEHFRKPVPPSPED
LSVICFTSGTTGDPKGAMITHQNIVSAAAFLKCVEHAYEPTPDDVAISYLPRAHMFERIVQ
AVVYSCGARVGFFQGDIRLLADDMKTLKPTLFPAVPRLLNRIYDKVQNEAKTPLKKFLLKLA
VSSKFKELOKGIIIRHDSFDKLIFAKIQDSLGGRVRVIVTGAAPMSTSVMFFRAAMGCQVY
EAYGQTECTGGCTFTLPGDWTSGHGVGPACNYVKLEDVADMNYFTVNNEGEVCIKGTNVFK
GYLKDPPEKTQEALDSDGWLHTGDIGRWLPGNTLKIIDRKKNIFKLAQGEYIAPEKIENIYNR
SQPVQLQIFVHGESLRSSLGVVVVPDTDVLPSFAAKLGVKGSFEELCQNQVVREAILEDLQKI
GKESGLKTFEQVKAIFLHPEPFSIENGLLPTLKAKRGELSKYFRTQIDSPLYEHIQD
```

Important features:

Type II transmembrane domain:

amino acids 61-80

Putative AMP-binding domain signature.

amino acids 314-325

N-glycosylation site.

amino acids 102-105, 588-591 and 619-622



FIGURE 53

GGAGGC GGAGGCC CGCGAGCC GGGCCAGCAGTGAGGGCCCTAGCGGGGCCGAGCGGGG
CCC GGGGCCCTAAGCCATT CCTGAAGTCATGGGCTGGCCAGGACATTGGTACCCGCCAAT
CCGGT**ATG**GACGACTGGAAGCCAGCCCCCATCAAGCCCTTGGGGCTCGGAAGAACGG
AGCTGGTACCTAACCTGGAAGTATAAACTGACAAACCAGCGGGCCCTGCGGAGATTCTGTCA
GACAGGGCCGTGCTTCTGCTGGTACTGTCATTGTCAATATCAAGTTGATCCTGGACA
CTCGCGAGCCATCAGTGAAGCCAATGAAGACCCAGAGCCAGAGCAAGACTATGATGAGGCC
CTAGGCCGCTGGAGCCCCACGGCGAGAGCAGTGGTCCCCGGCAGGTGCTGGAGGATG
GGTGTATTCAAGTCGCAGCAAAGTATATGTGGCAGTGGATGGCACCCAGGTGCTGGAGGATG
AGGCCGAGCAGGGCCGGGCATCCATGTCATTGCTCAACCAGGCCACGGCCACGTG
ATGGCAAAACGTGTGTTGACACGTACTCACCTCATGAGGATGAGGCCATGGTCTATTCT
CAACATGGTAGCGCCGGCCAGTGCTCATCTGCACTGTCAAGGATGAGGGCTCCTCCACC
TCAAGGACACAGCCAAGGCTCTGCTGAGGAGCCTGGCAGCCAGGCTGCCCTGCCCTGGC
TGGAGGGACACATGGCCTCGTGGACGAAAAGGAGGTCCTGTCTGGGAGAACATT
TAAGTCACCTGCCCTCTTCTGGGGGACCCAGTCCTGCTGAAGACAGATGTGCCATTGA
GCTCAGCAGAACAGGGCAGAGTGCCTGGCAGACACAGAGCTGAACCGTGCAGGCCGGC
TTCTGCAGCAAAGTTGAGGGCTATGGAAGTGTATGCAGCTGCAAGGACCCACACCATCGA
GTTCAAGGCCACTCCAGACAACAAGGTCTCAATGTGCCCTGTCATTGCAG
GGAACCGACCCATTACCTGTACAGGATGCTCGCTCTGCTTCAAGCCCAGGGGTGTCT
CCTCAGATGATAAACAGTTTCTTGCAGGGCTACTATGAGGAACCCATGGATGTGGTGGCACT
GTTGGTCTGAGGGCATTCCAGCATACTCCCATCAGCATCAAGAATGCCCGCGTCTCAGC
ACTACAAGGCCAGCCTCACTGCCACTTCAACCTGTTCCGGAGGCCAAGTTGCTGTGGTT
CTGGAAGAGGACCTGGACATTGCTGTGGATTTCAGTTCTGAGGCCAATCCATCCACCT
ACTGGAGGAGGATGACAGCCTGACTGCATCTGCTGGAAATGACCAGGGTATGAACACA
CGGCTGAGGACCCAGCACTACTGTACCGTGTGGAGACCATGCCTGGCTGGCTGGTGCTC
AGGAGGTCTTGACAAGGAGGAGCTTGAGGCCAAGTGGCTACACCGGAAAAGCTCTGGGA
TTGGGACATGTGGATGCGGATGCCCTGAACACGCGGGGCCAGAGTGCATCATCCCTGACG
TTTCCCGATCCTACCAACTTGGCATCGTCGGCTCAACATGAATGGCTACTTCACGAGGCC
TACTTCAAGAACAGTCAACACGGTCCAGGTGTCCAGCTCAGGAATGTGGACAGTCT
GAAGAAAGAACGCTATGAAGTGGAGTTCACAGGCTGCTCAGTGAGGCTGAGGTTCTGGACC
ACAGCAAGAACCCCTGTGAAGACTCTTCTGCCAGACACAGAGGGCACACCTACGTGGCC
TTTATTGGAATGGAGAAAGATGATGACTTCACCACCTGGACCCAGCTGCCAAGTGCCTCCA
TATCTGGGACCTGGATGTGCGTGGCAACCACCGGGCTGTGGAGATTGTTGGAAAGAAGA
ACCACTTCTGGTGGTGGGCTCCGGCTTCCCCCTACTCAGTGAAGAACGCCACCCCTCAGTC
ACCCCAATTTCCTGGAGCCACCCCAAAGGAGGAGGGCAGGAGGCCAGAACAGAC
ATGAACCTCCTCCAGGACCCCTGCGGGCTGGTACTGTGACCCAGGCTGGCTAGCCCT
TCCCTCCATCCTGTAGGATTTGTAGATGCTGGTAGGGCTGGGCTACCTGTTTAACA
TGAGACTTAATTACTAACCTAACAGGGAGGGTCCCTGCTCCAACACCCCGTCCCTGAGTT
AAAAGTCTATTATTTACTCCTGTGGAGAACGGCAGGAGAGTACCTGGGAATCATTACG
ATCCCTAGCAGCTCATCCTGCCCTTGAATACCTCACTTCCAGGCCAGGCTGGCTCAGAAC
ACCTATTATTGACTGTCTGAGGCCCTGAAAACAGGCCAACCTGGAGGGCCTGGATTTC
TTTTGGGCTGGAATGCTGCCCTGAGGGTGGGCTGGCTCTACTCAGGAAACTGCTGTGCC
CAACCCATGGACAGGCCAGCTGGGCCACATGCTGACACAGACTCACTCAGAGAACCTTA
GACACTGGACCAGGCCCTCAGCCTCTTGTCCAGATTCAAAGCTGGATAAGTT
GGTCATTGATTAAGGAGAACCCCTGGGAAAAAAAAAAAAAA



54/249

FIGURE 54

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA61185
><subunit 1 of 1, 660 aa, 1 stop
><MW: 75220, pI: 6.76, NX(S/T): 0
MDDWKPSPLIKPFGARKKRSWYLTWKYKLTNQRALRRFCQTGAVLFLLVTIVNIKLILDTR
RAISEANEDPEPEQDYDEALGRLEPPRRRGSGPDRVLDVEVYSSRSKVVAVDGTIVLEDEA
REQGRGIHVIVLNQATGHVMAKRVFDTYSRHEDEAMVLFLNMVAPGRVLICTVKDEGSFHLK
DTAKALLRSLGSQAGPALGWRDTWAFVGRKGGPVFGEKHSKSPALSSWGDPVLLKTDVPLSS
AEEAECHWADTELNRRLRFCSKVEGYGSVCSCDKPTPIEFSPDPLPDNKVLNPVAVIAGN
RPNLYRMLRSLLSAQGVSPQMITVFIDGYEEPMDVVALFGLRGIQHTPISIKNARVSQHY
KASLTATFNLFPPEAKFAVVLEEDLDIAVDFFSFLSQSIHLLEEDDSLKYCISAWNDQGYEHTA
EDPALLYRVETMPGLGVLRRLSYKEELEPKWPTPEKLWDWDMWMRMPEQRRGRECIIPDVS
RSYHFGIVGLNMNGYFHEAYFKHKFNTVPGVQLRNDSLKEAYEVHRLLSEAEVLDHS
KNPCEDSFLPDTEGHTYVAFIRMEKDDDFTTWTQLAKCLHIWDLDVRGNHRLWRLFRKKNH
FLVVGVVPASPVKKPPSVTPIFLEPPPKEEGAPGAPEQT
```

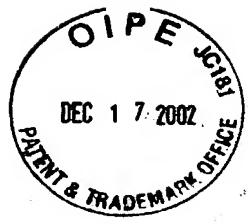
Important features of the protein:

Transmembrane domain:

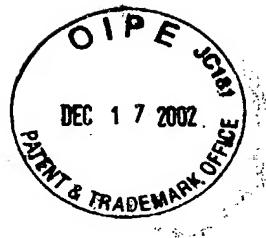
amino acids 38-55

Homologous region to Mouse GNT1

amino acids 229-660

**FIGURE 55**

CGGACGCGTGGGCTGCTGGGGAAAGGCCTAAAGAACTGGAAAGCCCCTCTCTTGAACCACAC
CTGTTAAAGAACCTAACGCACCATTTAAAGCCACTGGAAATTGTCTAGTGGTGTTGGGATGTTA
AAGGAGGGCAGAATGGATGATTCATCTCCATTAGCCTGCTCTGGCTATGTTGGGGATGTTA
CGTGGCCGGAATCATTCCCTGGCTGTTAATTCTCAGAGGAACGACTGAAGCTGGTACTGTTGG
GTGCTGGCCTCTGTGGAACTGCTCTGGCAGTCATCGTGCCTGAAGGAGTACATGCCCTTATGAA
GATATTCTGAGGGAAAACACCAAGCAAGTAAACACATAATGTGATTGCATCAGACAAAGCAGC
AGAAAAATCAGTGTCCATGAACATGAGCACAGCCACGACCACACAGCTGCATGCCATATTGGTG
TTCCCTCGTTCTGGGCTTCGTTCATGTTGCTGGGACAGATTGTAACCTCCATGTCATTCT
ACTGACGATCCAGAAGCAGCAAGGTCTAGCAATTCCAAACACCACGCTGGTCTGGTGTCCA
TGCTGCAGCTGATGGTGTGCTTGGGAGCAGCAGCATCTACTTCACAGACCAGTGTCCAGTTAATTG
TGTGTTGTGGAATCATGCTACATAAGGCACAGCTGCTTTGGACTGGTTCTTCTTGATGCATGCT
GGCTTAGAGCGGAATCGAACATCAGAAAGCACTTGCTGGTCTTGCAATTGGCAGCACCAGTTATGTCAT
GGTGACATACTTAGGACTGAGTAAGAGCAGTAAAGAAGCCCTTCAGAGGTGAACGCCACGGGAGTGG
CCATGCTTTCTGCGGGACATTCTTATGTTGCCACAGTACATGTCCTCCCTGAGGTGGCGGA
ATAGGGCACAGCCACAAGCCCAGTGCCACGGGAGGGAGAGGCCTCAGCCCTGGAAGTGGCAGCCCT
GGTTCTGGGTTGCCATCCCTCATCCTGTCAGTAGGACACCAGCATTAAATGTTCAAGGTCCAGC
CTTGGTCCAGGGCCCTTGCCATCCAGTGAGAACAGCCGGCACGTGACAGCTACTCACCTCCTCAGTC
TCTTGTCTCACCTTGCATCTACATGATTCTAGAGTCCAGAGGGGAGGGTGAAGGTTAAACCTG
AGTAATGGAAAAGCTTTAGAGTAGAACACATTACGTTGCAAGTTAGCTATAGACATCCATTGTT
TATCTTTAAAGGCCCTTGACATTGCGTTTAATATTCTCTTAACCTATTCTCAGGGAAAGATG
GAATTAGTTAAGGAAAAGAGGAGAACCTCATACTCACAATGAAATAGTGATTATGAAAATACAGT
GTTCTGTAATTAAAGCTATGTCCTTCTTAGTTAGAGGCTGCTACTTATCCATTGATT
AACATGGTCCCACCATGTAAGACTGGTCTTAGCATCTGCCACATGCGTTGATGGAAGGTATA
GCACCCACTCACTTAGATGCTAAAGGTGATTCTAGTTAATCTGGGATTAGGGTCAGGAAAATGATAGC
AAGACACATTGAAAGCTCTTTACTCAAAGAGATATCCATTGAAAAGGGATGTCTAGAGGGATT
TAAACAGCTCCTTGGCACGTGCCTCTGAATCCAGCCTGCCATTCCATCAAATGGAGCAGGAGG
TGGGAGGAGCTCTAAAGAGGTGACTGGTATTGTTAGCATCCTGTCAGTTCTCCTTGCAGAAT
ACCTGTCCTCACATTCTAGAGAGGCCAAGTCTAGTAGTTCTAGGCTTCTCAGGTTCTCCTTCAAGAA
CAGTCAGATCACAAAGTGTCTTGGAAATTAAAGGGATTAAATTAAAGTGAATTGGATGGTTAT
TGATATCTTGTAGTAGCTTTAAAAGACTACCAAAATGTATGGTTGTCCTTTTTGTTTT
TTTTTTTTAATTATTCTCTTAGCAGATCAGCAATCCCTCTAGGGACCTAAATAACTAGGTAGCTT
GGCAGACACTGTGTCCTCTCACATAACCACCTGTAGCAAGATGGATCATAAATGAGAAGTGGCTA
TTGATTTAAAGCTATTGGAATCATGTCCTGCTCTCGTCTTTGCTTTCTTCTAATT
TCCCTCTAGCCTCTCCCTGCCACAATTGCTGCTACTGCTGGTGTAAATTGTTGTTGGATGAATT
CTTATCAGGACAACCACTCTGAACTGTAATAATGAAGATAATAATCTTATTCTTATCCCTT
CAAAGAAATTACCTTGTGTCAAATGCCGTTGTTGAGCCCTAAAATACCACCTCCTCATGTTAA
ATTGACACAATCACAATCTGGTAATTAAACAAATTGAGATAGCAAAAGTGTAAACAGACTAGGATA
ATTTTTTTTCAATTGCAAAATTGTTGAAACCTGCTTGTCAAATAAGTGTATAATTGTT
TATTAATTATTCTTACTTCTATACCAATTCAAAACACATTACACTAAGGGGAAACCAAGACTAGTT
TCTTCAGGGCAGTGGACGTAGTAGTTGTAACCTGTTCTATGACGCATAAGCTAGCATGCCATTG
ATTATTCTCTCATGAATTGTCACTGGATCAGCAGCTGTTGAAATAAGCTGTGAGGCCCTGCT
GCCACAGTGAGGAAAGTAGCACAATAGGATACAGTTGTTGAGTCATTGGCAACAAATTGATACA
ATTTTACTACCAAGAGAAGGTATAGTATGGAAAGTCCAAATGACTCCCTGATTGGATGTTAACAGCT
GACTGGTGTGAGACTTGAGGTTCATCTAGCCTTCAAAACTATATGGTTGCCAGATTCTCTGG
AACTGACTTGTCAAATAATAGCAGATTGTTGCAAAAAAA



56/249

FIGURE 56

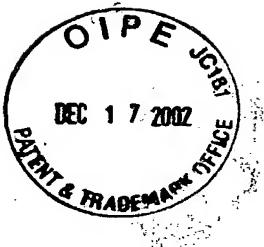
MDDFISISLLSLAMLVGCYVAGIIPLAVNFSEERLKLVTLGAGLLCGTALAVIVPEGVHAL
YEDILEGKHHQASETHNVIASDKAAEKS VVHEHEHSHDHTQLHAYIGVSLVLGFVFMLLVDQ
IGNSHVHSTDDPEAARSSNSKITTLGLVVHAAADGVALGAAASTSQTSVQLIVFVAIMLHK
APAAFGLVSFLMHAGLERNRIRKHLLVFALAAPVMSMVTYLGLSKSSKEALSEVNATGVAML
FSAGTFLYVATVHLPEVGGIGHSHKPDATGGRGLSRLEVAALVLGCLIPPLILSVGHQH

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 37-56, 106-122, 211-230, 240-260, 288-304



U.S. PATENT AND TRADEMARK OFFICE

57/249

FIGURE 57

GCTCGAGGCCGGCGGCGGGAGAGCGACCCGGCGGCCTCGTAGCGGGGCCGGATCCC
CGAGTGGCGGCCGGAGCCTCGAAAAGAGATTCTCAGCGCTGATTGAGATGATGGCCTGG
GAAACGGCGTCGCAGCATGAAGTCGCCGCCCTCGTGTGCCGCCCTGGTGGCCTGCATC
ATCGTCTGGGCTCAACTACTGGATTGCGAGCTCCGGAGCGTGACCTCCAGACACGGAT
CATGGAGCTGGAAGGCAGGGTCCGCAGGGCGGCTGCAGAGAGAGGGGCCGTGGAGCTGAAGA
AGAACGAGTTCCAGGGAGAGCTGGAGAAGCAGCGGGAGCAGCTTGACAAAATCCAGTCAGC
CACAACTCCAGCTGGAGAGCGTCAACAAGCTGTACCAGGACGAAAAGGCGTTTGGTGA
TAACATCACCACAGGTGAGAGGCTCATCCGAGTGCTGCAAGACAGTTAAAGACCCCTGCAGA
GGAATTACGGCAGGCTGCAGCAGGATGTCCCTCAGTTCAAAGAACAGACCAACCTGGAG
AGGAAGTCTCCTACGACCTGAGCCAGTGATCAATCAGATGAAGGAGGTGAAGGAACAGTG
TGAGGAGCGAATAGAAGAGGTACCAAAAAGGGGAATGAAGCTGTAGCTTCAGAGACCTGA
GTGAAAACAACGACCAGAGACAGCAGCTCCAAGCCCTCAGTGAGCCTCAGCCCAGGCTGCAG
GCAGCAGGCCTGCCACACACAGAGGTGCCACAAGGGAAACGTGCTGGTAACAGCAA
GTCCCAGACACCAGCCCCAGTTCCGAAGTGGTTGGATTCAAAGAGACAAGTTGAGAAAG
AGGAAACCAATGAGATCCAGGTGGTAATGAGGAGCCTCAGAGGACAGGCTGCCGCAGGAG
CCAGGCCGGAGCAGGTGGGAAGACAGACCTGTAGGTGGAAGAGGCTCGGGGAGCCGG
AGAACTGGGCCAGACCCACAGGTGCAGGCTGCCCTGTCAGTGAGCCAGGAAAATCCAGAGA
TGGAGGGCCCTGAGCGAGACCAGCAGAAACTGAGAGGAGAAGATGACTACAACATGGATGAAAA
GCCGGGGAGGGAGAAACCAGCAGAAACTGAGAGGAGAAGATGACTACAACATGGATGAAAA
TGAAGCAGAATCTGAGACAGACAAGCAAGCAGCCCTGGCAGGGAAATGACAGAAACATAGATG
TTTTAATGTTGAAGATCAGAAAAGAGACACCATAAATTACTTGATCAGCGTAAAAGCGG
AATCATACACTTGAATTGAACTGGAATCACATATTCACAAACAGGGCGAAGAGATGACTA
TAAAATGTTCATGAGGGACTGAATACTGAAAATGTACTAAATAAAATGTACATCTGA



58/249

FIGURE 58

MMGLGNRGRSMKSPPLVLAALVACIIVLGFNYWIASSRSVDIQTRIMELEGRVRRAAAERGA
VELKKNEFQGELEKQREQLDKIQSSHNFQLESVNKLQYQDEKAVLVNNITTGERLIRVLQDQL
KTLQRNYGRLQQDVLQFQKNQTNERKFSYDLSQCINQMKEVKEQCEERIEEVTKKGNEAVA
SRDLSENNQRQQQLQALSEPQPRLQAAGLPHTEPQGKGNVLGNSKSQTPAPSSEVVLDSKR
QVEKEETNEIQVVNEEPQRDRLPQEKGREQVVEDRPVGGRGGAGELGQTPQVQAALSVSQ
ENPEMEGPERDQLVIPDGQEEEQEAAGEGRNQQKLRGEDDYNMDENEAESETDKQAALAGND
RNIDVFNVEDQKRDTINLLDQREKRNHTL

Signal peptide:

amino acids 1-29



DEC 17 2002

59/249

FIGURE 59

GGATGAGAAAGCCTCAGTGTGCTCTGGCCTGGGCTGCTTCTACGCTGGCATTGCCCTTC
CCAGTGCTTCTGTCACCGTTGGAGCTACCAACCATAAGCAGCTGCCAAGAGCCCCCAGGCCCTGGTCCC
TGCCATGGGGAGCCAAGGAAACCTGGGCTGCTGGATGGCTCCGATTTCGCGGGTTGTGTTGGTGTGA
TAGATGCTCTGCATTGACTTCGCCAGCCCCAGCATTACACGTGCCAGAGAGCCTCTGTCTCCCTACCC
TCCTGGCAAACTAAGCTCCCTGCAGAGGATCCTGGAGATCAGCCCCACCATGCCGGCTCTACCGATCTCAGG
TTGACCCCTTACCAACCAGCAGCGCTCAAGGCCCTACCACTGGCTCACTGCCAACCTTATTGATGCTG
GTAGTAACCTGCCAGCCAGCAGCATTGGAAAGACAATCTATTAGCAGCTCACAGTGAGGAAGCGTGTAG
TCTTCATGGGAGATGATACTGGAAAGACCTTCCCTGGCTTCTCCAAAGCTTCTTCCATCTTCA
ATGTCAGAGACCTAGACACAGTGGACAATGGCATCCTGGAACACCTCACCCACCATGGACAGTGGTAATGGG
ACGTGCTGATTGCTCACTTCCGGGTGTTGACCAACTGTGGGCCACAAGCATGGCCCTCACCAACCTGAAATGGCA
AGAAAATCTAGCCAGATGGACCAAGGGTGTCCAGGGACTTGTGGAGCGTCTGGAGAATGACACACTGTGGTAGTGG
CTGGGACCATGGGATGACCAACATGGAGACCATGGAGGGACAGTGAGCTGGAGGTCTCAGTGCTCTTTC
TGTATAGCCCCACAGCAGTCTTCCCCAGCACCAGAGGAGGAGGGAGGAGGTGATTCTCAAGTTAGCCTTGTG
CCACGCTGGCCCTGCTGGGCTGCCATCCATTGGAAATATGGGAAATGATGGCTGAGCTATTCTCAG
GGGGTGGAGGACTCCAGCCCCACTCCTGCTTAGCCCAAGCCTCAGCTCTCCATCTCAAGTGCTCAGCAGGTGT
CCCGATTCTCATACCTACTCAGCTGCTACTCAGGACCTCAAGCTAAGGAGCTTCACTCAGTGAGAACCTCT
TCTCCAAGGCTCTGCTGACTACCAGTGGCTTCTCCAGAGCCCCAAGGGGCTGAGGCGACACTGCCACTGTGA
TTGCTGAGCTGAGCAGTCTCTGCGGGAGCTGGGCCATGTGCATCAGTCTGGCTCGTTCTCTGGTCC
GCATGGGGGGGTAUTGCTCTCTGGCTGCTTCTGCTTATCTGCTGCTGGCATCTCAGTGGCAATATCCC
CAGGCTTCCATTCTGCCCTACTCCTGACACCTGTGGCTGGGCTGGTTGGGCCATAGCGTATGCTGGAC
TCCTGGAACTATTGAGCTGAAGCTAGATCTAGTGCTTAGGGCTGTGGCTGAGCTGAGCTCATTCTCCCT
TTCTGTGGAAAGCCTGGCTGGCTGGGCTCAAGAGGCCCTGGCAACCTGTTCCCATCCCTGGCCCGTCC
TGTTACTCCTGCTGTTCTGGCTGTGTTCTCTGATAGTTTGTTGAGCTGAGGCCAGGGCCACCCCC
TCCCTTGGGCTCATTCTGCTCTGGTGTCCAGCTCAGGGAGGCCAGCTGCCACCTAAGCTAC
TCACAATGCCCGCCTGGCACTTCAGCCACAACAAACCCCCACGGCACAATGGTGATATGCCCTGAGGCTTG
GAATTGGGTTGCTTTATGTAACAGGCTAGCTGGCTTTCTACGCTGGCCCTGAAGAGACACCTGTTGGC
CCTCTCCCTGGCTGAGCTCTGGCATTCCATGGTGGTGGCGAGGCAAGAAATTATGGTATGGAGCTTGTG
CGGCGCTGGTGGGCTGTTAGCTGCCCTGGCTGTCCAGCTCAGGGAGGCCAGCTGCCACCTGGG
CCATGCTCTTGTGCGCTGGGACTGCCCTAATGGCATTGGTACTGCTGCCACTGGGATTGGCGT
CAGATGAGGCTCCCCCGTCTCGGGCTCTGGTCTCTGGGCTATCCATGGTGTGCTGCCCTGGGCTGTAGCAGGG
TGGCTGCTTCAGGGCTGCCCTGCTGCTGGAGCTGGCTCTGGAGCTGACAGTGTGAGGCTGGGAGGCC
GGACCAAGGACTGCTCTACTCCCTCTCAGGCCCCCCTACTCTCAAGCTGACTGGATTATGTGGCC
TCTACCGACACATGCAGGAGGAGTCCGGGGCGGTTAGAGAGGACCAATCTCAGGGTCCCTGACTGTGGCT
CTTATCAGTTGGGAGTGTACTCAGCTGCTATGGTACAGCCCTACCCCTGGCTTCCACTCTGCTGT
TGCATGCCAGCGCATGCCCTGTGTTCTGCTTCTGAGAGCTCCCTACATCTGCTTGCT
CTGGGATACCGCTCACCAACCCCTGGTCTTTACTGTGCCATGGCAGGAGCTCGGCTGGGCCCTCATGGCCA
CACAGACCTTCTACTCCACAGGCCACAGCCTGCTTCCAGCCATCCATTGGCATGCAGCTTGTGGGATTCC
CAGAGGGCATGGCTCTGACTTGGCTGCCCTGCTTAGGGAGCCAACACCTTGCCTCCACCTCCTCT
TGCAGTAGGTTGCCACTGCTCCCTGCTCTGGCTTCTGAGAGCTGAGGAGTCAAGGGCTGCCAGAGACAGCAGC
CCCCAGGGAATGAAGCTGATGCCAGAGCTCAGACCCGAGGGAGGAAGAGGAGGCCACTGATGGAGATGCCCTGGGG
ATGCGCCTCAGCACTTCTATGCAAGCAGTCTGCACTGGGCTCAAGTACCTTATCCTGGTATTGAGATT
TGGCTGCTTGGCAGGCCCTCATCTGGCAGGCTCATCTCATGGTCTGGAAAGTGTGTTGGCC
TTAGTCTGAGGCTGGGCTTCAATTGTGAGCAGCTGGGACTTCTCTGGGATAGCTTGGTGTAGAGAGTGGATGGT
CTGTGAGCTCTGGTCAAGCAGCTATTCTGGGCCAGCAGAGGTTAGCCTAGTGTGATTACTGGCACTTGGCT
ACAGAGAGTGTGGAGAACAGTGTAGGCTGGCTGTACAGGACTGATGGAGATCTGCAAGACAGGCTCACCC
TCTTACTATCATGCAGCCAGGGCCGCTGACATCTAGGACTTCATTATTCTATAATT
CAGGACCAAGTGGAGTA
TGATCCCTAACTCCTGATTGGATGCACTGAGGGACAAGGGGGGGCTCAGGGAGTGGAAATAAAAGGCC
GCCGTGGTACTGCACCTATAATCCAGCACTTGGGAGGGCAGAGGAGGATTGCTGGTCCCAGGAGTTCA
AGACCAGCCTGTGGAACATAACAAGACCCGTCTACTATTAAAAAAAGTGAATAAAATGATAATAT



60/249

FIGURE 60

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62809
<subunit 1 of 1, 1089 aa, 1 stop
<MW: 118699, pI: 8.49, NX(S/T): 2
MQKASVLLFLAWVCFLFYAGIALFTSGFLLTRLELTNHSSCQEPPPGPSLPWGSQGKPGACW
MASRFSRVVLVLIDALRFDFAQPQHSHVPREPPVSLPFLGKLSSLQRILEIQPHHARLYRSQ
VDPPTTTMQRALKALTGSPLTFIDAGSNFASHAIVEDNLIKQLTSAGRVVFMGDDTWKDLF
PGAFSKAFFFPSFNVRDLDTVDNGILEHLYPTMDSGEWDVLIAHFLGVDHCGKHGPHEM
AKKLSQMDQVIQGLVERLENDTLLVVAGDHGMTTNGDHGGDSELEVSAALFLYSPTAVFPST
PPEEPEVIPQVSLVPTLALLGLPIFGNIGEVMAELSGGEDSQPHSSALAQASALHLNAQ
QVSRLFHTYSAATQDLQAKELHQLQNLFSKASADYQWLLQSPKGAEATLPTVIAELQQFLRG
ARAMCIESWARFSLVRMAGGTALLAASCFCILLASQWAISPGBFCPLLTPVAWGLVGAIA
YAGLLGTIELKLDLVLLGAVAAYSSFLPFLWKAWAGWGSKRPLATLFPPIPGLVLLLFRLA
VFFSDSFVVAEARATPFLLGSFILLLVQHLWEGQLLPPKLLMPRLGTSATTNPPRHNGAY
ALRLGIGLLLCTRLAGLFHRCPEETPVCHSSPWLSPLASMVGGRAKNLWYGACVAALVALLA
AVRLWLRRYGNLKSPEPPMLFVRWGLPLMALGTAAYWALASGADEAPRRLRVLSGASMVLP
RAVAGLAASGLALLWKPVTVLVKAGAGAPRTRTVLTPFSGPPTSQADLDYVVPQIYRHMQE
EFRGRLERTKSQGPLTVAAYQLGSVYSAAMVTALTLLAFPLLLHAERISLVFLLLFLQSFL
LLHLLAAGIPVTPGPFTVPWQAVSAWALMATQTFYSTGHQPVFPAIHWHAASFVGFPEGHGS
CTWLPALLVGANTFASHLLFAVGCPLLLWPFLCESQGLRKQQPPGNEADARVRPEEEEEP
LMEMRLRDAPQHFYAALLQLGLKYLFILGIQILACALAASIIRRHLMVWKVFAPKFIFEAVG
FIVSSVGLLLGIALVMRVDGAVSSWFRQLFLAQQR
```

Important features:

Signal peptide:

amino acids 1-16

Transmembrane domains:

amino acids 317-341, 451-470, 481-500, 510-527, 538-555, 831-850,
1016-1034, 1052-1070

Leucine zipper pattern.

amino acids 843-864

N-glycosylation sites.

amino acids 37-40, 268-271

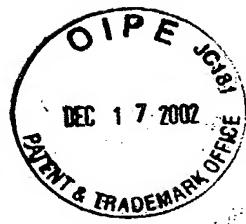


2025 RELEASE UNDER E.O. 14176

61/249

FIGURE 61

TGCCGCTGCCGCCGCTGCTGCTGTTGCTCCTGGCGGCCTGGGGACGGCAGTCCCTGT
GTCTCTGGTGGTTGCCTAACACTGAAACATCACCTTCTTATCCATCAACATGAAGAATGT
CCTACAATGGACTCCACCAGAGGGCTTCAAGGAGTTAAAGTTACTTACACTGTGCAGTATT
TCATCACAAATTGGCCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTCTGTTGT
CCTGACAGCTCCAGAGAAGTGGAAAGAGAAATCCAGAAGACCTCCTGTTCCATGCAACAAA
TATACTCCAATCTGAAGTATAACGTGTCTGTGTTGAATACTAAATCAAACAGAACGTGGTCC
CAGTGTGTGACCAACCACAGCTGGTGTCACCTGGCTGGAGCCGAACACTTTACTGCGT
ACACGTGGAGTCCTCGTCCCAGGGCCCCCTGCCGTGTCAGCCTCTGAGAAGCAGTGTG
CCAGGACTTGAAAGATCAATCATCAGAGTTCAAGGCTAAATCATCTTCTGGTATGTTTG
CCCATATCTATTACCGTGTGTTCTTTCTGTGATGGCTATTCCATCTACCGATATATCCA
CGTTGGCAAAGAGAAACACCCAGCAAATTGATTTGATTTATGGAAATGAATTGACAAAAA
GATTCTTGTGCCTGCTGAAAAAAATCGTGATTAACTTATCACCCCTCAATATCTGGATGAT
TCTAAAATTCTCATCAGGATATGAGTTACTGGAAAAAGCAGTGATGTATCCAGCCTAA
TGATCCTCAGCCCAGCGGGAACCTGAGGCCCCCTCAGGAGGAAGAGGAGGTGAAACATTAG
GGTATGCTTCGCATTGATGGAAATTGGCTTGACTCTGAAGAAAACACGGAAGGTACTTCT
CTCACCCAGCAAGAGTCCCTCAGCAGAACAAATACCCCGATAAAACAGTCATTGAATATGA
ATATGATGTCAGAACCACTGACATTGCGGGGCCTGAAGAGGCCAGGAGCTCAGTTGCAGG
AGGAGGTGTCCACACAAGGAACATTGGAGTCGCAGGCAGCGTTGGCAGTCTGGCCCG
CAAACGTTACAGTACTCATACACCCCTCAGCTCCAAGACTTAGACCCCTGGCGCAGGAGCA
CACAGACTCGGAGGGAGGGCCGGAGGAAGAGCCATCGACGACCCCTGGCGACTGGATCCCC
AAACTGGCAGGCTGTGATTCCTCGCTGTCCAGCTCGACCAGGATTCAAGAGGCTGCGAG
CCTTCTGAGGGGATGGCTCGAGAGGAGGGCTTCTATCTAGACTCTATGAGGAGCCGGC
TCCAGACAGGCCACCAGGAGAAAATGAAACCTATCTCATGCAATTGAGGAATGGGGGT
TATATGTCAGATGGAAAACTGATGCCAACACTCCCTTGCCTTGTGCAAAC
AAAGTGAGTCACCCCTTGATCCAGCCATAAAGTACCTGGATGAAAGAAGTTTTCCAGT
TTGTCAGTGTCTGTGAGAATTACTTATTCCTTCTATTCTCATAGCACGTGTGATTG
GTTCATGCATGTAGGTCTCTAACATGATGGGGCCTCTGGAGTCAGGGCTGGCCGGT
TGTTCTATGCAGAGAAAGCAGTCAATAATGTTGCCAGACTGGGTGCAGAATTATTCAAGG
TGGGTGT



62/249

FIGURE 62

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62815
<subunit 1 of 1, 442 aa, 1 stop
<MW: 49932, pI: 4.55, NX(S/T): 5
MSYNGLHQQRVFKELKLLTLCSSISSLQIGPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQ
QIYSNLKYNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRRAQPSEKQ
CARTLKQDQSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRYIHVGKEHPANLILYGNFED
KRFFVPAEKIVINFITLNISDDSKISHQDMSSLGKSSDVSSLNDPQPSGNLRPPQEEEVKH
LGYASHLMEIFCDSEENTEGTSLTQQESLSRTIPPDKTVIEYEYDVRTTDICAGPEEQEQLSL
QEEVSTQGTLLESQAALAVLGPQTLQYSYTPQLQDLDPLAQEHTDSEEGPEEPSTTLVDWD
PQTGRLCIPSLSSFDQDSEGCEPSEGGLGE EGLLSRLYEEPAPDRPPGENETYLMQFMEEW
GLYVQMEM
```

Important features:

Signal peptide:

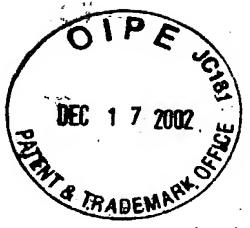
amino acids 1-28

Transmembrane domain:

amino acids 140-163

N-glycosylation sites.

amino acids 71-74, 80-83, 89-92, 204-207, 423-426



63/249

FIGURE 63

CGGACGCGTGGCGGACGCGTGGCGGACGCGTGGGTCTCTGCAGGGAGACGCCAGCCTGCG
TCTGCC**ATG**GGGCTCGGGTTGAGGGCTGGGGACGTCCCTCTGCTGACTGTGCCACCGCCCT
GATGCTGCCGTGAAGCCCCCGCAGGCTCCTGGGGGCCAGATCATGGGGGCCACGAGG
TGACCCCCACTCCAGGCCCTACATGGCATCCGTGCCTCGGGGCCAACATCACTGCGGA
GGCTTCCTGCTGCGAGCCCCTGGTGGTCTCGGCCCGCCACTGCTCAGGCCACAGAGACCT
CCGCACTGGCCTGGTGGTGCCTGGCGCCACGTCCCTGAGTACTGCGGAGCCCACCCAGCAGG
TGTTTGGCATCGATGCTCTCACCAACGCACCCGACTACCACCCATGACCCACGCCAACGAC
ATCTGCCTGCTGCGGCTGAACGGCTCTGCTGTCCTGGGCCCTGCAGTGGGCTGCTGAGGCT
GCCAGGGAGAAGGCCAGGCCCCCACAGCGGGACACGGTGCCGGTGGCTGGCTGGGCT
TCGTGTCTGACTTTGAGGAGCTGCCCTGGACTGATGGAGGCCAAGGTCCGAGTGCTGGAC
CCGGACGTCTGCAAACAGCTCCTGGAAGGCCACCTGACACTTACCATGCTCTGCCACCCGAG
TGGGACAGCCACAGACGGGCTTCTGCTGCCGACTCCGAGGGCCCTGGTGTGCAGGA
ACCGGGCTCACGCCCTGTTCTCGGCCCTGGATCTGGACGTGGTCCGGAGCAGTCC
GTGTACACGCAGGTGTCCGCCCTTGATGGCTGGACGTGGTCCGGAGCAGTCC
CCAGCCGGCCCCCTGCCTGGACCAACAGGCCAGGAGAAGGCC**TGA**GCCACAACCT
TGGGCATGCAAATGAGATGCCGCTCCAGGCCTGGAATGTTCCGTGGCTGGGCCCCACGGG
AAGCCTGATGTTAGGGTTGGGTGGACGGCAGCGGTGGGCACACCCATTCCACATGCA
AAGGGCAGAAGCAAACCCAGTAAATGTTAAGTACAACAAAAAAAAGAAA



64/249

FIGURE 64

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62845
><subunit 1 of 1, 283 aa, 1 stop
><MW: 30350, pI: 9.66, NX(S/T): 2
MGLGLRGWGRPLLTVATALMLPVKPPAGSWGAQIIGGHEVTPHSRPYMASVRFGGQHHCGGF
LLRARWVVSAAHCFSHRDLRTGLVVLGAHVLSTAEPQQVFGIDALTTHPDYHPMTHANDIC
LLRLNGSAVLGPAVGLLRLPGRRARPPTAGTRCRVAGWGFVSDFEELPPGLMEAKVRVLDPD
VCNSSWKGHLTLMCTRSGDHSRRGFCSDSGGPLVCRNRAHGLVSFSGLWC GDPKT PDVY
TQVSAFVAWIWDVVRRSSPQPGPLPGTTRPPGEAA
```

Signal peptide:

amino acids 1-30

FIGURE 65

GAGCTACCCAGGCGGCTGGTGTGCAGCAAGCTCCGCCGACTCCGGACGCCTGACGCCTGA
CGCCTGTCCCCGGCCCGGCA**TG**AGCCGCTACCTGCTGCCGCTGTCGGCGCTGGGCACGGTAG
CAGGCGCCGCCGTGCTCAAGGACTATGTCACC GGTTGGGGCTTGCCCCAGCAAGGCCACC
ATCCCTGGGAAGACGGTCATCGTGACGGCGCCAACACAGGCATCGGAAGCAGACCGCCTT
GGA ACTGCCAGGAGAGGAGGCAACATCATCCTGGCCTGCCAGACATGGAGAAGTGTGAGG
CGGCAGCAAAGGACATCCGCCGGGAGACCCCTCAATCACCATGTCAACGCCGGCACCTGGAC
TTGGCTCCCTCAAGTCTATCCGAGAGTTGCAGCAAAGATCATTGAAGAGGGAGGAGCAGT
GGACATTCTAACAAACGCCGGGTGTGATGCCGTGCCCTGGACCACCGAGGACGGCT
TCGAGATGCAGTTGGCGTTAACCAACCTGGTCACTTCTCTTGACAAACTGCTGCTGGAC
AAGCTGAAAGCCTCAGCCCCTCGCGGATCATCAACCTCTCGTCCCTGGCCATGTTGCTGG
GCACATAGACTTTGACGACTTGAACGGCAGACGAGGAAGTATAACACCAAAGCCGCCTACT
GCCAGAGCAAGCTGCCATCGTCCCTTCAGCACCACACTCGGGCCATCTTCTGGCTGCTGGTCAAGA
GGTGTGACTGTCAACGCCCTGCACCCCGCGTGGCCAGGACAGAGCTGGCAGACACACGGG
CATCCATGGCTCCACCTCTCCAGCACCACACTCGGGCCATCTTCTGGCTGCTGGTCAAGA
GCCCGAGCTGCCGCCAGCCCAGCACATACTGCCGTGGCGAGGAACGGGATGTT
TCCGGAAAGTACTCGATGGACTCAAACAGAAGGCCCGGCCCTGGCTAGAGGCTCCCTGTGA
GGTGGCCCGAGGCTTGGCTGAAAGTGCCCGCTGGTGGCTTAGAGGCTCCCTGTGA
GGGAGCAGCCCTCCCCAGA**TAA**CCCTGGAGCAGATTGAAAGCCAGGATGGCGCTCCAG
ACCGAGGACAGCTGTCCGCCATGCCCGCAGCTTCTGGCACTACCTGAGCCGGAGACCCAG
GACTGGCCGCCATGCCCGCAGTAGGTTCTAGGGGGCGGTGCTGCCGCAGTGGACTGGC
CTGCAGGTGAGCACTGCCCGGCTCTGGCTGGTCCGTCTGCTCTGCCAGCAGGGAG
AGGGGCCATCTGATGCTTCCCTGGGAATCTAAACTGGGAATGGCCGAGGAGGAAGGGGCTC
TGTGCACCTGCAGGCCACGTCAAGGAGAGCCAGCGGTGCCTGTCGGGGAGGGTCCAAGGTGC
TCCGTGAAGAGCATGGCAAGTTGTCTGACACTTGGTGGATTCTTGGTCCCTGTGGACCT
TGTGCATGCATGGCCTCTCTGAGCCTGGTTCTCAGCAGTGAGATGCTCAGAATAACTG
CTGTCTCCATGATGGTGTGGTACAGCGAGCTGTTGCTGGCTATGGCATGGCTGTGCCGG
GGTGTGCTGAGGGCTTCTGTGCCAGAGCCCAGCCAGAGAGCAGGTGCAGGTGTCACTCCC
GAGTTCAAGGCTCTGCACGGCATGGAGTGGGAACCCACCAAGCTGCTGCTACAGGACCTGGGA
TTGCCTGGACTCCCACCTCCTATCAATTCTCATGGTAGTCCAAACTGCAGACTCTCAAAC
TTGCTCATTT



66/249

FIGURE 66

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64842

><subunit 1 of 1, 331 aa, 1 stop

><MW: 35932, pI: 8.45, NX(S/T): 1

MSRYLLPLSALGTVAGAAVLLKDYVTGGACPSKATIPGKTVIVTGANTGIGKQTALELARRG
GNIILACRDMEKCEAAAKDIRGETLNHHVNARHLDLASLKSIREFAAKIIEEEERVDILINN
AGVMRCPHWTTEDGFEMQFGVNHLGHFLLTNLLDKLKASAPSRIINLSSLAHVAGHIDFDD
LNWQTRKYNTKAAYCQSKLAIVLFTKELSRRLLQGSGVTVNALHPGVARTELGRHTGIHGSTF
SSTTLGPIFWLLVKSPELAAQPSTYLVAAEELADVSGKYFDGLKQKAPAPEAEDEEVARRLW
AESARLVGLEAPSvreQPLPR

Signal peptide:

amino acids 1-17



100 200 300 400 500 600 700 800 900

67/249

FIGURE 67

GAAGTTCGCGAGCGCTGGC**ATG**TGGCCTGGGCGCGCTGGCGCGCTGCTGGCGGTGCTG
GCGCTCGGGACAGGAGACCCAGAAAGGGCTCGGGCTCGGGCGACACGTTCTCGGCCTGAC
CAGCGTGGCGCGCCCTGGCGCCCGAGCGCCGGCTGCTGGGCTGCTGAGGCGGTACCTGC
GCAGGGAGGAGGCGCGCTGCGGGACCTGACTAGATTCTACGACAAGGTACTTCTTGAT
GAGGATTCAACAAACCCCTGTGGCTAACCTCTGCTTGATTTACTCTCATCAAACGCCTGCA
GTCTGACTGGAGGAATGTGGTACATAGTCTGGAGGCCAGTGAGAACATCCGAGCTCTGAAGG
ATGGCTATGAGAAGGTGGAGCAAGACCTTCAGCCTTGAGGACCTTGAGGGAGCAGCAAGG
GCCCTGATGCGGCTGCAGGACGTGTACATGCTCAATGTGAAAGGCCTGGCCCGAGGTGTCTT
TCAGAGAGTCACTGGCTCTGCCATCACTGACCTGTACAGCCCCAACGGCTCTTCTCA
CAGGGGATGACTGCTCCAAGTTGCAAGGTGGCTATGACATGGGGATTATTACCATGCC
ATTCCATGGCTGGAGGAGGCTGTCAGTCTCTCCAGGGATCTACGGAGAGTGGAAGACAGA
GGATGAGGCAAGTCTAGAAGATGCCTTGGATCACTTGGCTTTGCTTACAGCCCAGATAATAAGAGG
ATGTTTGTGTGCCCTCAGCCTCTCGGGAGTTCTCTCTACAGCCCAGATAATAAGAGG
ATGGCCAGGAATGCTTGAATATGAAAGGCCTTGGCAGAGAGCCCCAACCACGTGGTAGC
TGAGGCTGTACATCAGAGGCCAATATAACCCACCTGCAGACCAGAGACACCTACGAGGGC
TATGTCAGACCCCTGGGTCCCAGCCACTCTCTACCCAGATCCCTAGCCTCTACTGTTCTAT
GAGACCAATTCCAACGCCTACCTGCTGCTCCAGCCATCCGGAAGGAGGTATCCACCTGGA
GCCCTACATTGCTCTCTACCATGACTCGTCAGTGAUTCAGAGGCTCAGAAAATTAGAGAAC
TTGCAGAACCATGGCTACAGAGGTAGTGGCATCAGGGAGAAGCAGTTACAAGTGGAG
TACCGCATCAGCAAAAGTGCCTGGCTGAAGGACAATGTTGACCCAAAATGGTGACCCCTCAA
CCACCGCATTGCTGCCCTCACAGGCCTTGATGTCGGCCTCCCTATGCAGAGTATCTGCAGG
TGGTGAACATGGCATCGGAGGACACTATGAGCCTCACTTGACCATGCTACGTCACCAAGC
AGCCCCCTACAGAAATGAAGTCAGGAAACCGAGTTGCAACATTATGATCTATCTGAGCTC
GGTGGAAAGCTGGAGGAGCCACAGCCTCATCTATGCCAACCTCAGCGTGCCTGTGGTTAGGA
ATGCAGCACTGTTTGGTGAACCTGCACAGGAGTGGTAAGGGGACAGTGACACACTTCAT
GCTGGCTGCCTGTCCTGGTGGAGATAAGTGGTGGCAACAAGTGGATACATGAGTATGG
ACAGGAATTCCGCAGACCCCTGCAGCTCCAGCCCTGAAGAC**TGA**ACTGTTGGCAGAGAGAAC
TGGTGGAGTCTGTGGCTTCCAGAGAAAGCCAGGAGCCAAAAGCTGGGTAGGAGAGGAGAA
AGCAGAGCAGCCTCTGGAAAGAAGGCCTGTCAGCTTGCTGCTCGCAAATCAGAGGC
AAGGGAGAGGTTGTTACCAAGGGACACTGAGAATGTACATTGATCTGCCCAAGGCCACGGAA
GTCAGAGTAGGATGCACAGTACAAAGGAGGGGGAGTGGAGGCCTGAGAGGGAAAGTTCTGG
AGTTCAAGATACTCTGTTGGGAAACAGGACATCTCACAGTCTCAGGTTGATCAGTGGTC
TTTGGCACTTGAACCTTGACCAAGGGACCAAGAAGTGGCAATGAGGACACCTGCAGGAG
GGGCTAGCCTGACTCCCAGAACTTTAAGACTTCTCCCCACTGCCTCTGCTGCAGCCCAAG
CAGGGAGTGTCCCCCTCCCAGAAGCATATCCCAGATGAGTGGTACATTATATAAGGATT
TTAAGTTGAAAACAACTTCTTTCTTTGTATGATGGTTTTAACACAGTCATTAAGGATT
ATGTTATAAAATCAAAA



68/249

FIGURE 68

MGP GARLA ALLA VIAL ALG TD PER AARG DT FSALT SVARAL APERR LLG LL RRY LRGE EARL
RDL TRFY DKV LSL HED STT PVANPLLAFT LIKRL QSD W RVN VHS LEASE NI RALK DGY EK VE
QDL PAFED LE GAAR ALM RL QDV YM LV KGL ARG VF QR VT GS AIT DLY SPK RL FSL T GDDC FQ
VGK VAY DMG DYY HAI PW LEE AVS LFR GSY GEWKT EDEAS LED ALD HLA FAY FRAG NVSC ALS
LSREF LLYSPDN KRM ARNV LKY ERLLA E SPN HVV AEAVI QRP NIPHL QTR DTYE GLC QT LG S
QPT LYQ I PSL YCS YET NSNAY LLL QPIR KEV IHLE PYI ALYHDF VSD SEA QKIRE LAEP WL Q
RSV VAS GEK QL QVE YRISK SAWL KDT VDP KLVT LN HRIA ALT GLD VRPP YAEYL QV NYGIG
GHY EPH FDHAT SPSS PLY RMK SG NR VAT FM IYL SS VE AGGATAF IYAN LS VP VVR NA AL FW
NLH RS GEG DSD TLHAG CPV LVGD KVWANK WIHEY GQE FRR PCSS SPED

Signal peptide:

amino acids 1-19



FIGURE 69

GAGATAGGGAGTCTGGGTTAACGTTCCATCTCAGGAGCCCCTGCTCCCACCCCTAG
GAAGCCACCAGACTCCACGGTGTGGGCCAATCAGGTGGAATCGGCCCTGGCAGGTGGGCC
ACGAGCGCTGGCTGAGGGACCGAGCCGGAGAGCCCCGGAGCCCCCGTAACCCGCGCGGGAG
CGCCCAGGATGCCCGCGCGGGACTCGGAGCAGGTGCGCTACTGCGCGCTTCCTCACCTC
TGGCTCAAGTTTCACTTATCATCTATTCCACCGTGTCTGGCTGATTGGGCCCTGGTCCT
GTCTGTGGCATCTATGCAGAGGTTGAGCGGCAGAAATAAAAACCTTGAAAGTGCCTTCC
TGGCTCCAGCCATCATCCTCATCCTGGCGTGTGTCATGTTGTCATGGTCTCCTTCATTGGT
GTGCTGGCGTCCCTCCGTGACAACCTGTACCTTCTCCAAGCATTGTCATGTACATCCTGGAT
CTGCCTCATCATGGAGCTCATGGTGGCGTGGTGGCCTTGACCTCCCGAACAGACCATTG
ACTTCTGAACGACAACATTGAAAGAGGAATTGAGAAACTACTATGATGATCTGGACTTCAA
AACATCATGGACTTGTTCAGAAAAAGTTCAAGTGTGCTGGCGGGAGGACTACCGAGATTG
GAGCAAGAATCAGTACCAACCGACTGCAGTGCCCCTGGACCCCTGGCCTGTGGGTGCCCTACA
CCTGCTGCATCAGGAACACGACAGAAAGTTCAACACCATGTGTCATGAAACTATCGAC
AAGGAGCGTTTCAGTGTGCAGGATGTCATCTACGTGCGGGCTGCACCAACGCCGTGATCAT
CTGGTTCATGGACAACACCATCATGGCGTGCATCCTCTGGCATCCTGCTTCCCCAGT
TCCTGGGGGTGCTGCTGACGCTGCTGTACATCACCCGGTGGAGGACATCATGGAGCAC
TCTGTCAGTGATGGCTCCTGGGCCCGGTGCCAAGCCCAGCGTGGAGGCGGCAGGCACGGG
ATGCTGCTTGTGCTACCCCAAT**TAG**GGCCCAGCCTGCCATGGCAGCTCCAACAAGGACCGTC
TGGGATAGCACCTCTCAGTCAACATCGTGGGGCTGGACAGGGCTGCGGCCCTCTGCCACA
CTCAGTACTGACCAAAGCCAGGGCTGTGTGCTGTGTAGGTCCCACGCCCTGCCTC
CCCAGGGAGCAGACCTGGCCTCCCTAAGAGGCTTCCCCGAGGCAGCTCTGGAATCTGT
GCCACCTGGGGCCTGGGAACAAGGCCCTCTTCTCCAGGCCTGGCTACAGGGAGGGA
GAGCCTGAGGCTCTGCTCAGGGCCATTTCATCTGGCAGTGCCTGGCGTGGTATTCAA
GGCAGTTTAGCACCTGTAATTGGGAGAGGGAGTGTGCCCCCTGGGGCAGGAGGGAAGG
GCATCTGGGAAGGGCAGGAGGGAAGAGCTGTCCATGCAGCCACGCCATGCCAGGTTGGC
CTCTTCTCAGCCTCCAGGTGCCTTGAGCCCTCTGCAAGGGCGCTGCTTCTTGAGCCTA
GTTTTTTTACGTGATTTGTAACATTCACTTTGTACAGATAACAGGAGTTCTGAC
TAATCAAAGCTGGTATTCGGCATGTCTTATTCTGCCCCAACCAGTTGTTAA
TCAAACAATAAAACATGTTGTTGTTAAAAAA



70/249

FIGURE 70

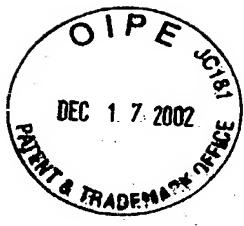
```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64863
><subunit 1 of 1, 294 aa, 1 stop
><MW: 33211, pI: 5.35, NX(S/T): 3
MPRGDSEQVRYCARFSYIWLKFSLIIYSTVFWLIGALVLSVGIYAEVERQKYKTLESAFLAP
AIILILLGVVMFMVSFIGVLASLRDNLYLLQAFMYILGICLIMELIGGVVALTFRNQTIDFL
NDNIIRGIENYYDDLDFKNIMDFVQKKFKCCGGEDYRDWSKNQYHDCSAPGPLACGVPYTCC
IRNTTEVVNTMCGYKTIDKERFSVQDVIVVRGCTNAVIIWFMDNYTIMACILLGILLPQFLG
VLLTLLYITRVEDIIMEHSVTDGLLGPGAKPSVEAGTGCLCYPN
```

Signal peptide:

amino acids 1-44

Transmembrane domains:

amino acids 22-42, 57-85, 93-116, 230-257



71/249

FIGURE 71

GAGGAGCGGGCCGAGGACTCCAGCGTGCCAGGTCTGGCATCCTGCACTTGCTGCCCTCTGA
CACCTGGGAAGATGGCCGGCCC GTGGACCTTCACCCTCTGTGGTTGCTGGCAGCCACC
TTGATCCAAGCCACCCCTCAGTCCC ACTGCAGTTCTCATCCTCGGCCAAAAGTCATCAAAGA
AAAGCTGACACAGGGAGCTGAAGGACCACAACGCCACCAGCATCCTGCAGCAGCTGCCGCTGC
TCAGTGCCATGCCGGAAAAGCCAGCCGGAGGCATCCCTGTGCTGGCAGCCTGGTAACACC
GTCCTGAAGCACATCATCTGGCTGAAGGT CATCACAGCTAACATCCTCCAGCTGCAGGTGAA
GCCCTCGCCAATGACCAGGAGCTGCTAGTCAAGATCCCCCTGGACATGGTGGCTGGATTCA
ACACGCCCTGGTCAAGACCATCGGAGTTCCACATGACGACTGAGGCCAAGCCACCATC
CGCATGGACACCAGTGCAAGTGGCCCCACCCGCTGGCCTCAGTGACTGTGCCACCAGCCA
TGGGAGCCTGCGCATCCA ACTGCTGTATAAGCTCTCCTCCTGGTAACGCCTAGCTAAC
AGGT CATGAACCTCCTAGTGCCATCCCTGCCAATCTAGTAAAAAACCAGCTGTGTCCCGTG
ATCGAGGCTTCCTCAATGGCATGTATGCAGACCTCCTGCAGCTGGTGAAGGTGCCATTTC
CCTCAGCATTGACCGTCTGGAGTTGACCTCTGTATCCTGCCATCAAGGGT GACACCATT
AGCTCTACCTGGGGCCAAGTTGGACTCACAGGGAAAGGTGACCAAGTGGTCAATAAC
TCTGCAGCTCCCTGACAATGCCACCCCTGGACAACATCCGTT CAGCCTCATCGTGAGTCA
GGACGTGGTGAAGCTGCAGTGGCTGCTGTGCTCTCCAGAAGAATT CATGGCCTGTTGG
ACTCTGTGCTCCTGAGAGTGCCATGGCTGAAGTCAAGCATGGGCTGATCAATGAAAAG
GCTGCAGATAAGCTGGATCTACCCAGATCGTGAAGATCTAACACTCAGGACACTCCGAGTT
TTTATAGACCAAGGCCATGCCAGGTGGCCAACTGATCGTGCTGGAGTGTCCCTCCA
GTGAAGCCCTCCGCCCTTGTTCACCTGGCATCGAACGCCAGCTCGGAAGCTCAGTTTAC
ACCAAAGGTGACCAACTTAACTCAACTTGAAATAACATCAGCTCTGATCGGATCCAGCTGAT
GAACTCTGGATTGGCTGGTCCAACCTGATGTTCTGAAAAACATCATCACTGAGATCATCC
ACTCCATCCTGCTGCCGAACCAGAATGGCAAATTAAAGATCTGGGTCCCAGTGTCAATTGGTG
AAGGCCTTGGGATTCGAGGCAGCTGAGTCCTCACTGACCAAGGATGCCCTGTGCTTACTCC
AGCCTCCTTGTGGAAACCCAGCTCCTGTCTCCAGTGAAGACTTGGATGGCAGCCATCAG
GGAAGGCTGGTCCCAGCTGGAGTATGGGTGTGAGCTCTAGACCATCCCTCTGCAAT
CAATAAACACTTGCCCTGTGAAAAAA



72/249

FIGURE 72

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64881
><subunit 1 of 1, 484 aa, 1 stop
><MW: 52468, pI: 7.14, NX(S/T): 3
MAGPWTFTLLCGLLAATLIQATLSPTAVLILGPKVIKEKLTQELKDHNATSILQQPLLSAM
REKPAGGIPLVLSLVNTVLKHIIWLKVITANILQLQVKPSANDQELLVKIPLDMVAGFNTPL
VKTIVEFHMTTEAQATIRMDTSASGPTRLVLSDCATSHGSLRIQLLYKLSFLVNALAKQVMN
LLVPSLPNLVKNQLCPVIEASFNGMYADLLQLVKVPISLSIDRLEFDLLYPAIKGDTIQLYL
GAKLLDSQGKVTKWFNNSAASLTMP LDNI PFSLIVSQDVVKAAVAAVLSPEEFMVLLDSVL
PESAHLRKSSIGLINEKAADKLGSTQIVKILTQDTPEFFIDQGHAKVAQLIVLEVFPSSEAL
RPLFTLGIEASSEAQFYTKGDQLILNLNNISSLRQLMNSGIGWFQPDVLKNIITEIIHSIL
LPNQNGKLRSRGVPVSLVKALGFEEAESSLTKDALVLT PASLWKPS SPV SQ

Important features of the protein:

Signal peptide:

amino acids 1-21

N-glycosylation sites.

amino acids 48-51, 264-267, 401-404

Glycosaminoglycan attachment site.

amino acids 412-415

LBP / BPI / CETP family proteins.

amino acids 407-457



73/249

FIGURE 73

GAGCGAAC**ATG**CAGCGC GTTGGCGTTGGTGTCTCTGTGACC ATGGTGGCGCTG
CTCATCGTTGCACGTTCCCTCAGCCTCTGCCAAAGAAAAGAAGGAGATGGTGTATCTGA
AAAGGTTAGTCAGCTGATGGAATGGACTAACAAAAGACCTGTAATAAGAATGAATGGAGACA
AGTTCCGTCGCCTGTGAAAGCCCACCGAGAAATTACTCCGTTATCGTCATGTTCACTGCT
CTCCA ACTGCATAGACAGTGTGCGTTGCAAGCAAGCTGATGAAGAATTCCAGATCCTGGC
AAACTCCTGGCGATACTCCAGTG CATTCAACACAGGATATTTTGCATGGTGGATT TG
ATGAAGGCTCTGATGTATTCAGATGCTAACATGAATT CAGCTCAACTTCATCAACTTT
CCTGAAAAGGAAACCAAACGGGTGATACATATGAGTTACAGGTGCGGGGTTTCAGC
TGAGCAGATTGCCCGGTGGATCGCCGACAGAACTGATGTCAATATTAGAGT GATTAGACCC
CAAATTATGCTGGTCCCCTATGTTGGATTGCTTTGGCTGTATTGGTGGACTTGTGTAT
CTTCGAAGAAGTAATATGGAATTCTCTTTAATAAAACTGGATGGCTTGCAGCTTGTG
TTTGTGCTTGCTATGACATCTGGTCAAATGTGGAACCATATAAGAGGACCA CATATGCC
ATAAGAATCCCCCACGGGACATGTGAATTATATCCATGGAAGCAGTCAGCCCAGTTGTA
GCTGAAACACACATTGTTCTCTGTTAATGGTGGAGTTACCTTAGGAATGGTGTCTTATG
TGAAGCTGCTACCTCTGACATGGATATTGAAAGCGAAAGATAATGTGTGGCTGGTATTG
GACTTGTGTATTATTCTCAGTTGGATGCTCTATTTTAGATCTAAATATCATGGCTAC
CCATACAGCTTCTGATGAGT**TAAA**AGGTC CCAGAGATATAGACACTGGAGTACTGGAA
ATTGAAAAACGAAAATCGTGTGTTGAAAAGAAGAATGCAACTTGATATTGTATTAC
CTCTTTTTCAAGT GATTAAATAGTTAACATTAACCAAGAAGATGTGTAGTGCCTTA
ACAAGCAATCCTCTGTCAAAATCTGAGGTATTGAAAATAATTATCCCTTTAACCTTCTCTT
CCCAGTGAACTTATGGAACATTAAATTAGTACAATTAGTATATTAAAAATTGTAAAA
CTACTACTTGT TTAGTTAGTTAGAACAAAAGCTAAA ACTACTTGTAACTGGTCATCTGAT
TTTATATTGCCTTATCCAAAGATGGGAAAGTAAGTCCTGACCAGGTGTTCCCACATATGCC
TGTTACAGATAACTACATTAGGAATTCTAGCTTCTAGCTCTCATCTTGTGTGGATGTGTAT
ACTTTACGCATCTTCTTTGAGTAGAGAAATTATGTGTGTCATGTGGTCTTGTGAAAATG
GAACACCATTCTCAGAGCACACGCTAGCCCTCAGCAAGACAGTTGTTCTCCTCCTCCT
GCATATT CCTACTGCGCTCCAGCCTGAGTGATAGAGT GAGACTCTGCTCAAAAAAAAGTA
TCTCTAAATACAGGATTATAATTCTGTTGAGTATGGTGTAACTACCTGTATTTAGAAA
GATTTCAGATTCCATCTCCTAGTTCTTTAAGGTGACCCATCTGTGATAAAAATA
TAGCTTAGTGCTAAAATCAGTGTAACTTACATGGCCTAAAATGTTCTACAAATTAGAGT
TTGTCACTTATTCCATTGTACCTAAGAGAAAATAGGCTCAGTTAGAAAAGGACTCCCTGG
CCAGGGCAGTGACTTACGCCCTGTAATCTCAGCACTTGGGAGGCCAGGCAGGAGTCAC
GAGGT CAGGAGTTCGAGACC ATCTGGCCAACATGGTGAACACCCGTCTACTAAAATAT
AAAAATTAGCTGGGTGTGGCAGGAGCCTGTAATCCCAGCTACACAGGAGGCTGAGGCAC
GAGAATCACTGAACTCAGGAGATGGAGGTTCA GTGAGGCCAGATCACGCCACTGCACTCC
AGCCTGGCAACAGAGCGAGACTCCATCTCAAAAAAAAAAAAAAA



74/249

FIGURE 74

MAARWRFWCVSVTMVALLIVCDVPSASAQRKKEMVLSEKVSQLMWEWTNKRPVIRMNGDKFR
RLVKAPPRNYSVIVMFTALQLHRCVCKQADEFQILANSWRYSSAFTNRIFFAMVDFDEG
SDVFQMLNMNSAPTFINFPAKGKPKRGDTYELQVRGFSAEQIARWIADRTDVNIRVIRPPNY
AGPLMLGLLLAVIGGLVYLRRSNMEFLFNKTGWAFAALCFVIALMTSGQMWNHIRGPPYAHKN
PTGHVNYIHSSQAQFVAETHIVLLFNGGVTLGMVLLCEAATSDMDIGKRKIMCVAGIGLV
VLFFSWMLSIFRSKYHGPYSFLMS

Signal peptide:

amino acids 1-29

Transmembrane domains:

amino acids 183-205, 217-237, 217-287, 301-321



FIGURE 75



76/249

FIGURE 76

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64885
<subunit 1 of 1, 536 aa, 1 stop
<MW: 61450, pI: 9.17, NX(S/T): 7
MLLLWVSVVAALALAVLAPGAGEQRRRAAKAPNVVLVSDSFGRFLTSHPGSQVVKLPFINF
MKTRGTSFLNAYTNSPICCPSSRAAMWSGLFTHLTESWNNFKGKLDPNYTTWMDVMERHGYRTQ
KFGKLDYTSGHSISNRVEAWTRDVAFLRQEGRPMVNLRNRTKVRVMERDWQNTDKAVNW
LRKEAINYTEPFVIYLGLNLPHYPSPSSGENFGSSTFHTSLYWLEKVSHDAIKIPKWSPLS
EMHPVDYYSSYTKNCTGRFTKKEIKNIRAFYYAMCAETDAMLGEIILALHQLDLLQKTIVIY
SSDHGELAMEHRQFYKMSMYEASAHVPLLMMGPGIKAGLQVSVNLVDIYPTMLDIAGIPL
PQNLSGYSLPLSSETFKNEHKVKNLHPPWILSEFHGCNVNASTYMLRTNHWKYIAYSDGAS
ILPQLFDLSSDPDELTNAVKFPEITYSLDQKLHSIINYPKVSASVHQYNKEQFIKWQSIG
QNYSNVIANLRWHQDWQKEPRKYENAIIDQWLKTHMNPRAV
```

Important features:

Signal peptide:

amino acids 1-15

N-glycosylation sites.

amino acids 108-111, 166-169, 193-196, 262-265, 375-378, 413-416,
498-501

Sulfatases proteins:

amino acids 286-315, 359-369, 78-97



77/249

FIGURE 77

GAGAGAAGTCAGCCTGGCAGAGAGACTCTGAAATGAGGGATTAGAGGTGTTCAAGGAGCAAG
AGCTTCAGCCTGAAGACAAGGGAGCAGTCCCTGAAGACGCTCTACTGAGAGGTCTGCC**ATG**
GCCTCTTGGCCTCCAACTTGTGGCTACATCCTAGGCCTCTGGGGCTTTGGGCACACT
GGTGCCATGCTGCCCTCAGCTGGAAAACAAGTTCTATGTCGGTGCCAGCATTGTGACAG
CAGTTGGCTTCTCCAAGGGCCTCTGGATGGAATGTGCCACACACAGCACAGGCATACCCAG
TGTGACATCTATAGCACCCCTCTGGCCTGCCGCTGACATCCAGGCTGCCAGGCCATGAT
GGTGACATCCAGTGAATCTCCTCCCTGGCCTGCATTATCTCTGTGGTGGGCATGAGATGCA
CAGTCTTCTGCCAGGAATCCCGAGCAAAGACAGAGTGGCGTAGCAGGTGGAGTCTTTTC
ATCCTTGGAGGCCTCCTGGGATTCAATTCTGTGCCTGGAATCTCATGGGATCCTACGGGA
CTTCTACTCACCACCTGGTGCCTGACAGCATGAAATTGAGATTGGAGAGGCTCTTACTTGG
GCATTATTCTTCCCTGTTCTCCCTGATAGCTGGAATCATCCTCTGCTTTCCCTGCTCATCC
CAGAGAAATCGCTCCAACTAACGATGCCAACCTCTGCCACAAGGAGCTC
TCCAAGGCCTGGTCAACCTCCAAAGTCAGAGTGGCTCAATTCTACAGCCTGACAGGGT
ATGTG**TGA**AGAACCAAGGGGCCAGAGCTGGGGGTGGCTGGTCTGTAAAAAACAGTGGACAG
CACCCCGAGGCCACAGGTGAGGGACACTACCAACTGGATCGTCAGAAGGTGCTGCTGAGG
ATAGACTGACTTTGCCATTGGATTGAGCAAAGGCAGAAATGGGGCTAGTGTAAACAGCATG
CAGGTTGAATTGCCAAGGATGCTGCCATGCCAGCCTTCTGTTTCCCTCACCTGCTGCTC
CCCTGCCCTAACGCCCCAACCTCAACTTGAAACCCCATTCCCTAACGCCAGGACTCAGAGG
ATCCCTTGCCTCTGGTTACCTGGACTCCATCCCCAACCCACTAACATCACATCCACTG
ACTGACCCCTCTGTGATCAAAGACCCCTCTCTGGCTGAGGTTGGCTTAGCTCATTGCTGG
GGATGGGAAGGAGAAGCAGTGGCTTGTGGCATTGCTCTAACCTACTTCTCAAGCTTCCC
TCCAAAGAAACTGATTGCCCTGGAACCTCCATCCACTCTGTTATGACTCCACAGTGTCC
AGACTAATTGTGCATGAACGTGAAATAAAACCATCCTACGGTATCCAGGGAACAGAAAGCAG
GATGCAGGATGGGAGGACAGGAAGGCAGCCTGGGACATTTAAAAAAATA



78/249

FIGURE 78

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64886
><subunit 1 of 1, 230 aa, 1 stop
><MW: 24549, pI: 8.56, NX(S/T): 1
MASLGLQLVGYILGLLGLLGTLVAMLLPSWKTSSYVGASIVTAVGFSKGLWMECATHSTGIT
QCDIYSTLLGLPADIQAAQAMMVTTSSAISSLACIISVVGMRCTVFCQESRAKDRVAVAGGVF
FILGGLLGFIPVAWLHGILRDFYSPLVPDSMKFEIGEALYLGISSLFSLIAGIILCFSCS
SQRNRSNYYDAYQAQPLATRSSPRPGQPPKVSEFNSYSLTGYV
```

Important features of the protein:

Signal peptide:

amino acids 1-24

Transmembrane domains:

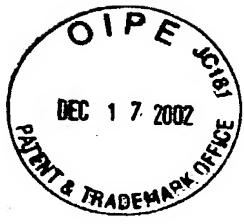
amino acids 82-102, 117-140, 163-182

N-glycosylation site.

amino acids 190-193

PMP-22 / EMP / MP20 family proteins.

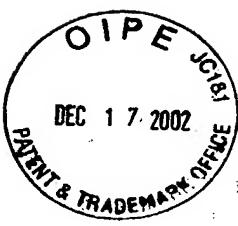
amino acids 46-59



79/249

FIGURE 79

GCAC TGCT GTCCC ATCAG CTGCT CTGA AGCT CCATG GTGCC CAGA ATCT CGCT CCTGC
TTAT GTGT CAGT CTGT CTCC CCTCTT GTCCA AGGG AAGTC ATCG CTCC GCTGG CTCAG
AACCAT GGCT GTGCC AGCCGGCACCCAGGT GTGGAGACAAGATCTACAACCC TTGGAGCAG
TGCT GTTACA ATGACGCCATCGTGTCCCTGAGCGAGACCCGCCAATGTGGTCCCCCTGCAC
CTTCTGGCCCTGCTTGAGCTCTGCTGTCTGATT CTTGCCTCACAAACGATT TGTTG
TGAAGCTGAAGGTTCAAGGT GTGA ATT CCCAGT GCCACTCATCTCCATCTCCAGTAAATGT
GAAAGCAGAAGACGTTTCCCTGA GAAGACATAGAAAGAAAATCAACTTCACTAAGGCATC
TCAGAACATAGGCTAAGGTAATATGTGTACCAAGTAGAGAAGCCTGAGGAATTACAAAATG
ATGCAGCTCCAAGCCATTGTATGGCCATGTGGGAGACTGATGGGACATGGAGAATGACAGT
AGATTATCAGGAAATAAATAAAGTGGTTTCCAATGTACACACCTGTAAAAA



80/249

FIGURE 80

MVPRIFAPAYVSVCLLLLCPREVIAPAGSEPWLQPAAPRCGDKIYNPLEQCCYNDIAIVSLSE
TRQCGPPCTFWPCFELCCLDSFGLTNDFVVKLKVQGVNSQCHSSPISSKCESRRRFP

Signal peptide:

amino acids 1-25



81/249

FIGURE 81

CTCCACTGCAACCACCCAGAGCC**ATG**GCTCCCCGAGGCTGCATCGTAGCTGTCTTGCATT
TTCTGCATCTCCAGGCTCCTCTGCTCACACGGAGCCCCAGTGGCCCCATGACTCCTTACCT
GATGCTGTGCCAGCCACACAAGAGATGTGGGGACAAGTTCTACGACCCCTGCAGCACTGTT
GCTATGATGATGCCGTCGTGCCCTTGGCCAGGACCCAGACGTGTGGAAACTGCACCTTCAGA
GCTCTGCTTGAGCAGTGTGCTGCCCTGGACCTTCATGGTGAAGCTGATAAACAGAACTGCGA
CTCAGCCCGGACCTCGGATGACAGGCTTGTGCGAGTCAGC**TAA**TGGAACATCAGGGAA
CGATGACTCCTGGATTCTCCTCTGGTGGGCTGGAGAAAGAGGCTGGTGTACCTGAGA
TCTGGGATGCTGAGTGGCTTTGGGGCCAGAGAAACACACACTCAACTGCCACTTCATT
CTGTGACCTGTCTGAGGCCACCCCTGCAGCTGCCCTGAGGAGGCCACAGGTCCCCTCTAG
AATTCTGGACAGCATGAGATGCGTGTGCTGATGGGGCCAGGGACTCTGAACCCCTCTGAT
GACCCCTATGGCCAACATCAACCCGGCACCAAGGCTGGCTGGGAACCCCTCACCCCT
TCTGTGAGATTTCCATCATCTCAAGTTCTTCTATCCAGGAGCAAAGCACAGGATCATAA
TAAATTATGTACTTTATAAATGAAAA



82/249

FIGURE 82

MAPRGCIVAVFAIFCISRLLC SHGAPVAPMTPYLM CQPHKRCGD KFYDPLQHCCYDDAVVP
LARTQTCGNCTFRVC FEQCCPWT FMVKLINQN CDSARTS DDL RLCRSVS

Signal peptide:

amino acids 1-24



U.S. PATENT AND TRADEMARK OFFICE

83/249

FIGURE 83

GGGGGCGGGTGCCTGGAGCACGGCGCTGGGGCCGCCGCAGCGCTCACTCGCTCGCACTCAG
TCGCAGGCTTCCCCGGCGCCGGCGTCCCGCCGCTCCCCGGCACCAGAAGTTCTCT
GCGGTCCGACGGCAGATGGGCGTCCCCACGGCCCTGGAGGCCAGCTGGCGCTGGGA
TCCCTGCTCTCGCTCTTCCTGGCTCGTCCCTAGGTCCGGTGGCAGCCTCAAGGTCGC
CACGCCGTATCCCTGTATGTCTGTCCCAGGGCAGAACGTCACCCACCTGCAGGCTCT
TGGGCCCTGTGGACAAAGGGCACGATGTGACCTCTACAAGACGTGGTACCGCAGCTCGAGG
GGCGAGGTGCAGACCTGCTCAGAGGCCGGCCATCCGAAACCTCACGTTCCAGGACCTCA
CCTGCACCATGGAGGCCACCAGGCTGCCAACACCAGCCACGACCTGGCTCAGGCCACGGC
TGGAGTCGGCCTCCGACCACCATGGCAACTCTCCATCACCATGCGAACCTGACCTGCTG
GATAGCGGCCTCTACTGCTGCCTGGTGGAGATCAGGCACCACACTCGGAGCACAGGGT
CCATGGTGCATGGAGCTGCAGGTGCAGACAGGCAAAGATGCACCATCCAACGTGTGGTGT
ACCCATCCTCCTCCCAGGATAGTGAAAACATCACGGCTGCAGCCCTGGCTACGGGTGCCTGC
ATCGTAGGAATCCTCTGCCTCCCCCTCATCCTGCTCCTGGTCTACAAGCAAAGGCAGGCAGC
CTCCAACGCCGTGCCAGGAGCTGGTGCAGACAGGCAAACATTCAAGGGATTGAAAACC
CCGGCTTGAGCCTCACCACTGCCAGGGATAACCGAGGCCAAAGTCAGGCACCCCTG
TCCTATGTGGCCCAGCGGCAGCCTCTGAGTCTGGCGCATCTGCTTCCGGAGCCAGCAC
CCCCCTGTCTCCTCCAGGCCCGGAGACGTCTTCTCCATCCCTGGACCCCTGCTCCCTGACT
CTCCAAACTTGAGGTCATCTAGCCCAGCTGGGGACAGTGGCTGTTGGCTGGTCTGG
GGCAGGTGCATTGAGCCAGGGCTGGCTCTGTGAGTGGCTCCTGGCCCTGGCCCTGGTTC
CCTCCCTCTGCTCTGGCTCAGATACTGTGACATCCAGAACGCCAGCCCTCAACCCCTC
TGGATGCTACATGGGATGCTGGACGGCTCAGCCCTGTTCCAAGGATTTGGGTGCTGAG
ATTCTCCCTAGAGACCTGAAATTCAACCAGCTACAGATGCCAAATGACTTACATCTTAAGAA
GTCTCAGAACGTCCAGCCCTCAGCAGCTCGTTCTGAGACATGAGCCTGGATGTGGCA
GCATCAGGGACAAGATGGACACTGGGCCACCCCTCCAGGCACCAAGACACAGGGCACGGT
GAGAGACTCTCCCCGTGGCCGCTTGGCTCCCCGTTTGGCCAGGGCTGCTCTGT
AGACTTCTCTTGACCACAGTGGCTCTGGGCCAGGCCTGCCACTGCCATGCC
ACCTTCCCAAGCTGCCTCTACCAGCAGTTCTCTGAAGATCTGCAACAGGTTAAGTCAAT
CTGGGGCTTCCACTGCCTGCATTCCAGTCCCCAGAGCTTGGTGGTCCGAAACGGGAAGTAC
ATATTGGGCATGGTGGCCTCCGTGAGCAAATGGTGTCTGGCAATCTGAGGCCAGGACAG
ATGTTGCCCAACCACTGGAGATGGTGTGAGGGAGGTGGTGGGCCCTCTGGGAAGGTGA
GTGGAGAGGGCAGCTGCCACACAAATGTCTGTCCACCCCTGGACACTTCTGAGTATGAAGC
ATTGCAAGGGTGCACACAATGTCTGTCCACCCCTGGACACTTCTGAGTATGAAGC
GCTATTAAAAACTACATGGGGAAAAAAAAAAAAAAAAAAAAAAAAGA



84/249

FIGURE 84

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64897
><subunit 1 of 1, 311 aa, 1 stop
><MW: 33908, pI: 6.87, NX(S/T): 6
MGVPTALEAGSWRWGSLLFALFLAASLGPVAAFKVATPYSLYVCPEGQNVTLCRLLGPVDK
GHDVTFYKTWYRSSRGEVQTCERRPIRNLTQDLHLHHGGHQAANTSHDLAQRHGLEASAD
HHGNFSITMRNLTLDSGLYCCLVVEIRHHHSEHRVHGAMELQVQTGKDAPSNCVVYPSSQ
DSENITAAALATGACIVGILCLPLILLVYKQRQAASNRRAQELVRMDSNIQGIENPGFEAS
PPAQGIPPEAKVRHPLSYVAQRQPSESGRHLLSEPSTPLSPPPGDVFFPSLDPPDSPNFEVI
```

Signal peptide:

amino acids 1-28

Transmembrane domain:

amino acids 190-216



85/249

FIGURE 85

CCACCGCGTCCGCGCTCTCCCTTCTGCTGGACCTTCCTCGTCTCCATCTCTCCCTCCT
TTCCCCGCGTTCTCTTCCACCTTCTCTTCTCCACCTTAGACCTCCCTGCCCTCC
TTCCCTGCCACCCTGCTTCCTGCCCTCTCCGACCCGCTCTAGCAGCAGACCTCCTGG
GGTCTGTGGGTTGATCTGTGGCCCTGTGCCTCCGTGTCCTTCGTCTCCCTCCGA
CTCCGCTCCCGGACCAGCGGCCTGACCCTGGGAAAGGATGGTCCCGAGGTGAGGGTCCTC
TCCTCCTGCTGGGACTCGCGCTGCTCTGGTTCCCCCTGGACTCCCACGCTCGAGCCGCC
AGACATGTTCTGCCTTTCCATGGGAAGAGATACTCCCCGGCGAGAGCTGGCACCCCTACT
TGGAGCCACAAGGCCTGATGTACTGCCTGCCTGTACCTGCTCAGAGGGGCCATGTGAGT
TGTTACCGCCTCCACTGTCCGCCTGTCCACTGCCACTGCCCTGTGACGGAGCCACAGCAATG
CTGCCCCAAGTGTGGAACCTCACACTCCCTCTGGACTCCGGGCCACCAAAGTCCTGCC
AGCACAACGGGACCATGTACCAACACGGAGAGATCTCAGTGCCATGAGCTGTTCCCCTCC
CGCCTGCCAACCAACAGTGTGCCTCTGCAGCTGCACAGAGGGCCAGATCTACTGCCCTCAC
AACCTGCCCGAACCAACAGGCTGCCAGCACCCCTCCACTGCCAGACTCCTGCTGCCAACGCT
GCAAAGATGAGGCAAGTGAGCAATCGGATGAAGAGGACAGTGTGCAGTCGCTCCATGGGTG
AGACATCCTCAGGATCCATGTTCCAGTGATGCTGGAGAAAGAGAGAGGCCGGCACCCAGC
CCCCACTGGCCTCAGGCCCTCTGAGCTTCATCCCTGCCACTCAGACCCAAGGGAGCAG
GCAGCACAACGTCAAGATCGTCTGAAGGAGAAACATAAGAAAGCCTGTGTCATGGCGGG
AAGACGTACTCCCACGGGAGGTGTGGCACCCGGCTTCCGTGCCCTGGCCCTTGCCCTG
CATCCTATGCACCTGTGAGGATGGCGCCAGGACTGCCAGCGTGTGACCTGTCCCACCGAGT
ACCCCTGCCGTACCCCGAGAAAGTGGCTGGGAAGTGCTGCAAGATTGCCAGAGGACAAA
GCAGACCCCTGCCACAGTGAGATCAGTTCTACCAGGTGTCCCAAGGCACCGGGCGGGCCT
CGTCCACACATCGGTATCCCAAGGCCAGACAACCTGCGCTTGCCTGGAACACGAGG
CCTCGGACTTGGTGGAGATCTACCTCTGGAAGCTGGAAAAGATGAGGAAACTGAGGCTCAG
AGAGGTGAAGTACCTGGCCAAGGCCACACAGCCAGAATCTTCACTGACTCAGATCAAGA
AAGTCAGGAAGCAAGACTTCCAGAAAGAGGGCACAGCACTCCGACTGCTCGCTGGCCCCAC
GAAGGTCACTGGAACGTCTCCTAGCCCAGACCCCTGGAGCTGAAGGTACGCCAGTCCAGA
CAAAGTGACCAAGACATAACAAAGACCTAACAGTTGCAGATATGAGCTGTATAATTGTTGTT
ATTATATATTAATAATAAGAAGTTGCATTACCCCTAAAAAAAAAAAAAA



86/249

FIGURE 86

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64902
><subunit 1 of 1, 451 aa, 1 stop
><MW: 49675, pI: 7.15, NX(S/T): 1
MVPEVRVLSSLLGALLWFPLDSHARARPDMFCLFHGKRYSPGESWHPYLEPQGLMYCLRCT
CSEGAHVSCYRLHCPPVHCPQPVTEPQQCCPKCVEPHTPSGLRAPPKSCQHNGTMYQHGEIF
SAHELFPSRLPNQCVLCSCTEGQIYCGLTTCEPGCPAPLPLPDSCCQACKDEASEQSDEED
SVQSLHGVRHPQDPCCSSDAGRKRGPGTPAPTGLSAPLSFIPRHFRPKGAGSTTVKIVLKEKH
KKACVHGGKTYSHGEVWHPAFRAFGPLPCILCTCEDGRQDCQRVTCPTEYPCRHPEKVAGKC
CKICPEDKADPGHSEISSTRCPKAPGRVLVHTSVSPSPDNLRRFALEHEASDLVEIYLWKLV
KDEETEAQRGEVPGPRPHSQNLPLSDQESQEARNPERGTALPTARWPPRSLERLPSPDPG
AEHGQSRQSDQDITKT
```

Signal peptide:

amino acids 1-25



87/249

FIGURE 87

CTAGCCTGCGCCAAGGGGTAGTGAGACCGCGCGAACAGCTTGC GGCTGC GGGGAGCTCCC
GTGGGCGCTCCGCTGGCTGTGCAGGC GGCC**ATGG**ATTCCTTGC GGAAAATGCTGATCTCAGT
CGCAATGCTGGCGCAGGGCTGGCGTGGCTACCGCCTCGTTATCGTGACCCCGGGAG
AGCGGCGGAAGCAGGAAATGCTAAAGGAGATGCCACTGCAGGACCCAGGAGCAGGGAGGAG
GCGCCAGGACCCAGCAGCTATTGCTGCCACTCTGCAGGAGGCAGCGACCACGCAGGAGAA
CGTGGCCTGGAGGAAGAACTGGATGGTGGCGCGAAGGC GGCGCAGC GGGAGGT CACCG**T**
GA GACCGGACTTGCCTCCGTGGCGCCGGACCTTGGCTGGCGCAGGAATCCGAGGCAGCC
TTTCTCCTCGTGGGCCAGCGGAGAGTCCGGACCGAGATA CCATGCCAGGACTCTCCGGGG
TCCTGTGAGCTGCCGTGGGTGAGCACGTTCCCCCAAACCCCTGGACTGACTGCTTAAGGT
CCGCAAGGC GGCCAGGGCCGAGACCGCAGTCGGATGTGGTGA ACTGAAAGAACCAATAAAA
TCATGTT CCTCCAAAAA AAAAAAAAAAAAAA AAAAAAAAAAAAAA AAAAAA
AAAAA



88/249

FIGURE 88

MDSLRKMLISVAMLGAGAGVGYALLVIVTPGERRKQEMLKEMPLQDPRSREEAARTQQLLLA
TLQEAATTQENVAWRKNWMVGEGGASGRSP

Signal peptide:

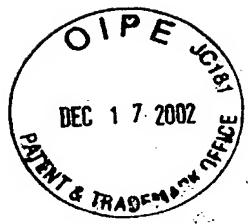
amino acids 1-18



89/249

FIGURE 89

CAGGAGAGAAGGCACCGCCCCACCCGCCTCCAAAGCTAACCCCTGGGCTTGAGGGGAAGA
GGCTGACTGTACGTTCTTCACTCTGGCACCCTCTCCAGGCTGCC**ATG**GGGCCAGCACC
CCTCTCCTCATCTGTTCTTGTCACTGGTCGGGACCCCTCCAAGGACAGCAGCACACCT
TGTGGAGTACATGGAACGCCGACTAGCTGCTTAGAGGAACGGCTGGCCAGTGCCAGGACC
AGAGTAGTCGGCATGCTGCTGAGCTGCCGACTCAGAACTGAGGCCGACACCCTCCGGGAGAGTGG
GTGGCAGAGAAGGAGCGGGAGGCAGTCAAGAACAGATGCTGCCACTGCTGGAG
TCGTCTGGAGCGGGAGGTAGACTATCTGGAGACCCAGAACCCAGCTCTGCCCTGTAGAGT
TTGATGAGAAGGTGACTGGAGGCCCTGGGACCAAAGGCAAGGAAAGAAGGAATGAGAAGTAC
GATATGGTACAGACTGTGGCTACACAATCTCAAGTGAAGATCAATGAAGATTCTGAAGCG
ATTGGTGGCCCAGCTGGTCTATGGACCAAGGATCCACTGGGCAAACAGAGAAGATCTACG
TGTTAGATGGGACACAGAACAGACACAGCCTTGTCTCCAAAGGCTGCGTACTTCACCCTT
GCCATGGCTGCCGGAAAGCTTCCGAGTCGGCTGCCCTCCCTGGTAGGCACAGGGCA
GCTGGTATATGGTGGCTTCTTATTGCTCGGAGGCCTCCTGGAAGACCTGGTGGAGGTG
GTGAGATGGAGAACACTTGAGCTAATCAAATTCCACCTGGCAAACCGAACAGTGGTGGAC
AGCTCAGTATTCCAGCAGAGGGCTGATCCCCCTACGGCTGACAGCAGACACCTACAT
CGACCTGGTAGCTGATGAGGAAGGTCTTGGCTGTCTATGCCACCCGGAGGATGACAGGC
ACTTGTCTGGCCAAGTTAGATCCACAGACACTGGACACAGAGCAGCAGTGGACACACCA
TGTCCCAGAGAGAACATGCTGAGGCTGCCTTGTCACTGTGGACCCCTATGTCGTCTATAA
CACCGTCCTGCCAGTCGGCCCGCATCCAGTGCTCCTTGTAGGCCAGCGGACCCCTGACCC
CTGAACGGCAGCACTCCCTATTTCAGATATGGTGCCTGCCATGCCAGCCTCCGCTAT
AACCCCGAGAACGCCAGCTATGCCCTGGGATGATGGCTACCAGATTGTCTATAAGCTGGA
GATGAGGAAGAAAGAGGAGGAGGTT**TGA**GGAGCTAGCCTGTTTGATCTTCACTC
CCATACATTATATTATCCCCACTAAATTCTTGTCTCATTCTCAAATGTGGCCAG
TTGTGGCTCAAATCCTCTATTTAGCCAATGGCAATCAAATTCTTCAGCTCCTTGT
TCATACGGAACTCCAGATCCTGAGTAATCCTTGTAGAGCCGAAGAGTC
TTCCCTCCTGCTCCTGCCCATGTCAACAAATTCAAGGCTAAGGATGCCAGGCCAG
GCTCTAACCTTGTATGCCAGGGCCAGGGAGCAGGCAGCAGTGTCTCCCTCAGAGTG
ACTTGGGAGGGAGAAATAGGAGGAGACGTCCAGCTGTCTCTTCCACTCCTCC
TCAGTGTCTGAGGAACAGGACTTCTCCACATTGTTGTATTGCAACATTGATTAAA
AGGAAAATCCACAAAAAAA
AAAAAAAAAAAAAAA
AAAAAAA



90/249

FIGURE 90

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64905
<subunit 1 of 1, 406 aa, 1 stop
<MW: 46038, pI: 6.50, NX(S/T): 2
MGPSTPLLILFLLSGPLQGQQHHLVEYMERRLAALEERLAQCQDQSSRHAELRDFKNKM
LPLLEVAKEREALRTEADTISGRVDRLEREVDYLETQNPALPCVEFDEKVTGGPGTKKGKR
RNEKYDMVTDCGYTISQVRSMKILKRFGGPAGLWTKDPLGQTEKIVLDGTQNDTAFVFPR
RDFTLAMAARKASRVRVFPFWVGTLVYGGFLYFARRPPGRPGGGEMENTLQLIKFHLAN
RTVVVDSSVFPAGEGLIPPYGLTADTYIDLVADEEGLWAVYATREDDRHLCLAKLDPQTLDTEQ
QWDTPCPRENAEAASFVICGTLVYVYNTRPASRARIQCSFDASGTLTPERAALPYFPRRYGAH
ASLRYNPRERQLYAWDDGYQIVYKLEMRKKEEEV
```

Important features:

Signal peptide:

amino acids 1-21

N-glycosylation sites.

amino acids 177-180, 248-251



91/249

FIGURE 91

GACAGCTGTCTCGATGGAGTAGACTCTCAGAACAGCGCAGTTGCCCTCCGCTACGCAG
AGCCTCTCCGTGGCTTCCGCACCTTGAGCATTAGGCCAGTTCTCCTCTCTAATCCAT
CCGTCACCTCTCCTGTATCCGTTCCATGCCGTGAGGTCCATTACAGAACACATCCATGG
CTCTCATGCTCAGTTGGTTCTGAGTCTCCTCAAGCTGGATCAGGGCAGTGGCAGGTGTT
GGGCCAGACAAGCCTGTCCAGGCCTGGTGGGGAGGACGCAGCATTCTCCTGTTCCCTGTC
TCCTAAGACCAATGCAGAGGCCATGGAAGTGCAGGTTCTCAGGGCCAGTTCTCTAGCGTGG
TCCACCTCTACAGGGACGGGAAGGACCAGCCATTATGCAGATGCCACAGTATCAAGGCAGG
ACAAAAACTGGTGAAGGATTCTATTGCGGAGGGCGCATCTCTGAGGCTGGAAAACATTAC
TGTGTTGGATGCTGGCCTCTATGGGTGCAGGATTAGTTCCCAGTCTTACTACCAGAAGGCCA
TCTGGGAGCTACAGGTGTCACTGGCTCAGTCCCTCAGTCCCTCACGGGATATGTT
GATAGAGACATCCAGCTACTCTGTCACTGGCTGGTCCCCGGCCACAGCGAAGTG
GAAAGGTCCACAAGGACAGGATTGTCCACAGACTCCAGGACAAACAGAGACATGCATGGCC
TGTTTGATGTGGAGATCTCTCTGACCGTCCAAGAGAACGCCGGAGCATATCCTGTTCCATG
CGGCATGCTCATCTGAGCCGAGAGGTGGAATCCAGGGTACAGATAGGAGATACTTTTCGA
GCCTATATCGTGGCACCTGGCTACCAAAGTACTGGGAATACTCTGCTGTGGCCTATTTTG
GCATTGTTGGACTGAAGATTTCTTCCAAATTCCAGTGGAAAATCCAGGGAACTGGAC
TGGAGAAGAAAGCACGGACAGGCAGAATTGAGAGACGCCGGAAACACGCAGTGGAGGTGAC
TCTGGATCCAGAGACGGCTACCCGAAGCTCTGCGTTCTGATCTGAAAATGTAACCCATA
GAAAAGCTCCCCAGGAGGTGCCTCACTCTGAGAAGAGATTACAAGGAAGAGTGTGGTGGCT
TCTCAGAGTTCCAAGCAGGGAAACATTACTGGAGGTGGACGGAGGACACAATAAGGTG
GCGCGTGGAGTGTGCCGGATGATGTGGACAGGAGGAAGGAGTACGTGACTTGTCTCCCG
ATCATGGTACTGGTCCTCAGACTGAATGGAGAACATTGTATTCACATTAAATCCCCGT
TTTATCAGCGTCTTCCCCAGGACCCACCTACAAAATAGGGTCTCCTGGACTATGAGTG
TGGGACCATCTCCTTCTTCAACATAAAATGACCACTCCCTTACAGGAGGAAAGACTCCC
TTGAAGGCTTATTGAGGCCCTACATTGAGTATCCGTCCTATAATGAGCAAAATGGAAC
ATAGTCATCTGCCAGTCACCCAGGAATCAGAGAAAGAGGCCCTTGGCAAAGGGCTCTGC
AATCCCAGAGACAAGCAACAGTGAGTCCTCCTCACAGGAACCCACGCCCTCCCCAGGG
GTGAAATGTAGGATGAATCACATCCCACATTCTTCTTAGGGATATTAAGGTCTCTCCCA
GATCCAAAGTCCCGCAGCAGCCGGCAAGGTGGCTTCCAGATGAAGGGGACTGGCCTGTCC
ACATGGGAGTCAGGTGTATGGCTGCCCTGAGCTGGAGGAAGAAGGCTGACATTACATT
AGTTGCTCTCACTCCATCTGGCTAAGTGATCTTGAAATACCACTCTCAGGTGAAGAACCG
TCAGGAATTCCCATCTCACAGGCTGTGGTAGATTAAGTAGACAAGGAATGTGAATAATGC
TTAGATCTTATTGATGACAGAGTGTATCCTAATGGTTGTTCATTATATTACACTTCAGTA
AAAAAA



U. S. PATENT AND TRADEMARK OFFICE

92/249

FIGURE 92

MALMLSIVSLLKLGSQWQVFGPDKPVQALVGEDAFAFSCFLSPKTNAEAMEVRFFRGQFSS
VVHLYRDGKDQPFMQMPQYQGRTKLVKDSIAEGRISLRLENITVLDAGLYGCRISSQSYYQK
AIWELQVSALGSVP LISITGYVDRDIQLLCQSSGWFP RPTAKWKGPQGQDLSTDRTNRDMH
GLFDVEISLTQENAGSISCSMRHAHLSREVESRVQIGDTFFEPISWHLATKVLGILCCGLF
FGIVGLKIFFSKFQWKIQAE LDWRRKHGQAE LRDAK HAVEVTLDPETAHPKLCVSDLKTVT
HRKAPQE VP HSEKRFTRKS VVASQSFQAGKHYWEVDGGHNKRWRVGVCRDDVDRRKEYVTLS
PDHGYWVLRLNGEHLYFTLNPRFISVFPRTPPTKIGVFLDYECGTISFFNINDQSLIYTLTC
RFEGLLRPYIEYPSYNEQNGTPIVICPVTQESEKEASWQRASAI PETSNSESSSQATTPFLP
RGEM

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 239-255



93/249

FIGURE 93

CGCATGGTGCGCCGGTGGCGGTGGCGGCTGGCGAGGCTTCCTGGTCGGATTGCA
ACGAGGAGAAGATGACTGACCAACCGACTGGCTGAATGAATGAATGGCGGAGCCGAGCGC
CATGAGGAGCCTGCCGAGCCTGGCGGCCCTGCCCTGTTGCTGCCGCCGCCGCC
CGCTGCCCTCAGCCGCTCGCGGGGAATGTCACCGGTGGCGGCCGCCGCC
GACCGCTGCCGGCCCCGGGTTGCCGGCGAGCCCAGCCACCCCTCCCTAGGGCAGCGC
TCCCACGGCCCAGGCCCCGAGGACCGGGCCCCGCGGCCACCGTCCACCGACCCCTGGCTG
CGACTTCTCCAGCCCAGTCCCCGGAGACCACCCCTTTGGCGACTGCTGGACCCCTTTCC
ACCACCTTCAGGCGCCGCTCGGCCCTGCCGACCACCCCTCCGGCGGCCGAACGCACTTC
GACCACCTCTCAGGCGCCGACCAGACCCGCGCGACCACCCCTTCGACGACCACGGCC
CGCCGACCACCCCTGTAGCGACCACCGTACCGGCCACGACTCCCCGGACCCGACCC
GATCTCCCCAGCAGCAGAACAGCAGCGTCTCCCCACCCACCTGCCACCGAGGCCCC
TTCGCCTCCTCCAGAGTATGTATGTAAGTGTCTGTGGTTGAAAGCCTGAATGTGAATCGCT
GCAACCAGACCACAGGGCAGTGTGAGTGTGGCCAGGTTATCAGGGCTTCACTGTGAAACC
TGCAAAGAGGGCTTTACCTAAATTACACTCTGGCTCTGCAAGGACCATCTGGTTAAACAAAG
ACATGGAGCTCTCAGCATACCGTCAACAGG**TAA**GCAACAGAGGGTGAACGTGAAGTTATT
TTATTTAGCAAGGGAAAAAAAAGGCTGCTACTCTCAAGGACCATCTGGTTAAACAAAG
GAGGATGAGGGTCATAGATTACAAAATTTATATACTTTATTCTCTTACTTTATATGT
TATATTAATGTCAGGATTAAAAACATCTAATTACTGATTAGTTCTTCAAAAGCACTAG
AGTCGCCAATTTCTGGATAATTCTGTAAATTCTGAAAGGCTTCAAGGATTTGAGGAAATT
AAATCTGCTTCTGGAAAGGGCTTCAGGCATGAAACCTGCTAGGAGGTTAGAAATGTTCTT
ATGTTATTAAATACCATGGAGTTGAGGAAATTGTTGTTGGTTATTCTCTCTA
ATCAAAATTCTACATTGTTCTGGACATCTAAAGCTTAACCTGGGGTACCTAATT
TTTAACTAGTGGTAAGTAGACTGGTTTACTCTATTACCAAGTACATTGAGACCAAAAG
TAGATTAAGCAGGAATTATCTTAAACTATTATGTTATTGGAGGTAATTAACTAGTGG
ATAATGTAAGTGTATCTAACGATTGCCTGTACTGCACTGAAAGTAATTATTCTTGCAC
TATGTGAGGCACCTGGCTTTGGACCCCAAGTCAAAAAAACTGAAGAGACAGTATTAAAT
AATGAAAAAAATAATGACAGGTTACTCAGTGTAAACCTGGGTATAACCCAAGATCTGCTGC
CACTTACGGAGCTGTGTTCTGGCAAGTAATTCTTCACTGAGCTGTTCTCTCAAG
GTTGTTGTGAAGATTAATGAGTTGATATATAAAATGCCTAGCACATGTCACTCAATAA
TTCTGGTTGTTAATTCAAAGGAATTATGGACTGAAATGAGAGAACATGTTAAAGA
ACTTTAGCTCCTGACAAAGAAGTGCTTATACCTTAGCACTAAATATTAAATGCTTTA
TAAATGATATTACTGTTATGGAATTATGTATCATATTGTAGTTATTAAAATGAGAAG
AGGCTGGCGCGGTGGCTACGCCGTAACTCCTAGCACTTGGGAGGCCAAGGCAGGTGGAT
CACTTGAGGCCAGGAGTTCTAGATGAGCCTGGCCAGCACAGTGAACACCCGTCTACTAAA
AATACAAACAAATTAGCTGGCGTGGTGGCACACACCTGTAGTCCAGCTACTCGGGAGGCT
GAGGCAGGAGAATCGGTTGAACCCGGGAGGTGGAGGTTGCACTGAGCTGAGATCGCGCCACT
GCACTCCAGCCTGGTGAGAGAGGGAGACTCTGTCTAAAAAAAAAAAAAA



94/249

FIGURE 94

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64952
><subunit 1 of 1, 258 aa, 1 stop
><MW: 25716, pI: 8.13, NX(S/T): 5
MRSLPSLGGALLCAAAAAAVASAASAGNVTGGGGAAGQVDASPGPGLRGEPSHPFPRATA
PTAQAPRTGPPRATVHRPLAATSPAQSPETTPLWATAGPSSTTFQAPLGPSPTPPAAERTS
TTSQAPTRPAPTTLSTTGPAPTTPVATTVPAPTTPRTPTPDLPSSNSVLPTPPATEAPS
SPPPEYVCNCSVVGSLNVNRCNQTTGQCECRPGYQGLHCETCKEGFYLNYTSGLCQPCDCSP
HGALSIPCNR
```

Important features of the protein:

Signal peptide:

amino acids 1-25

N-glycosylation sites.

amino acids 30-33, 172-175, 195-198, 208-211, 235-238

EGF-like domain cysteine pattern signature.

amino acids 214-226.



95/249

FIGURE 95

TGCGGCAGTGTAGACCTGGGAGGATGGGCGGCCTGCTGGCTGCTTTCTGGCTTGG
TCTCGGTGCCAGGGCCCAGGCCGTGTGGTGGAAAGACTGGACCTGAGCAGCTTCTGGG
CCCTGGTACGTGCTTGCCTGGCTCCGGAAAAGGGCTTGCCATGGAGAAGGACATGAA
GAACGTCGTGGGGTGGTGGTACCTCACTCCAGAAAACAACCTGCGGACGCTGTCCTCTC
AGCACGGCTGGGAGGGTGTGACCAGAGTGTATGGACCTGATAAACCGAAACTCCGGATGG
GTGTTGAGAATCCCTCAATAGCGTGCTGGAGCTCTGGGTGCTGCCACCAACTCAGAGA
CTATGCCATCATCTTCACTCAGCTGGAGTTGGGGACGAGCCCTAACACCGTGGAGCTGT
ACAGTCTGACGGAGACAGCCAGGCCAGGAGGCATGGGCTTCAACAGTGGAGCAGGAGC
CTGGGCTTCCTGTACAGTAGCAGGCCAGCTGCAGAAGGACCTCACCTGTGCTCACAGAT
CCTTCTGTGAGTGCTGCGTCCCCAGTAGGGATGGCGCCCACAGGGTCTGTGACCTCGGCCA
GTGTCCACCCACCTCGCTCAGCGGCTCCGGGCCAGCACCAGCTCAGAATAAGCGATT
CACAGCA



96/249

FIGURE 96

MGGLLLAAFLALVSPRAQAVWLGRLDPEQLLGPWYVLAVASREKGFAMEKDMKNVVGVVVT
LTPENNLRTLSSQHGLGGCDQSVMMDLIKRNSGWVFENPSIGVLELWVLATNFRDYAIIFTQL
EFGDEPFNTVELYSLTETASQEAMGLFTKWSRSLGFLSQ

Signal peptide:

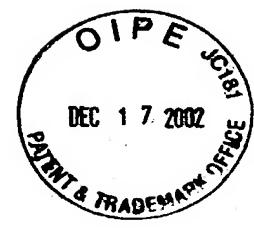
amino acids 1-20



97/249

FIGURE 97

AACAGACGTTCCCTCGCGGCCCTGGCACCTCTAACCCCAGAC**ATG**CTGCTGCTGCTGCTGCC
CCTGCTCTGGGGAGGGAGAGGGCGGAAGGACAGACAAGTAAACTGCTGACGATGCAGAGTT
CCGTGACGGTGCAGGAAGGCCTGTGTCCATGTGCCCTGCTCCTCTCCTACCCCTCGCAT
GGCTGGATTTACCCCTGGCCCAGTAGTCATGGCTACTGGTCCGGAAAGGGCCAATACAGA
CCAGGATGCTCCAGTGGCCACAAACAACCCAGCTCGGGCAGTGTGGGAGGAGACTCGGGACC
GATTCCACCTCCTGGGGACCCACATACCAAGAATTGCACCCCTGAGCATTGAGAGATGCCAGA
AGAAGTGTGATGCGGGGAGATACTTCTTCGTATGGAGAAAGGAAGTATAAAATGGAATTATAA
ACATCACCGGCTCTGTGAATGTGACAGCCTGACCCACAGGCCAACATCCTCATCCCAG
GCACCCCTGGAGTCCGGCTGCCCTCAGAATCTGACCTGCTCTGTGCCCTGGCCTGTGAGCAG
GGGACACCCCCCTATGATCTCCTGGATAGGGACCTCCGTGTCCCCCTGGACCCCTCCACAC
CCGCTCCTCGGTGCTCACCTCATCCCACAGCCCCAGGGACCATGGCACCCAGCCTCACCTGTC
AGGTGACCTTCCCTGGGCCAGCGTGACCAACGAACAAGACCGTCCATCTAACGTGTCCCTAC
CCGCCTCAGAACTGACCATGACTGTCTTCCAAGGAGACGGCACAGTATCCACAGTCTTGGG
AAATGGCTCATCTGTCACTCCCAGAGGGCAGTCTCTGCCTGGTCTGTGCAGTTGATG
CAGTTGACAGCAATCCCCCTGCCAGGCTGAGCCTGAGCTGGAGAGGCCTGACCCCTGTGCCCT
TCACAGCCCTCAAACCCGGGGTGCTGGAGCTGCCTGGTGCACCTGAGGGATGCAGCTGA
ATTCACCTGCAGAGCTCAGAACCCCTCTCGGCTCTCAGCAGGTCTACCTGAACGTCTCCCTGC
AGAGCAAAGCCACATCAGGAGTGACTCAGGGGGTGGTCGGGGAGCTGGAGCCACAGCCCTG
GTCTTCCCTGTCCTCTGCGTCATCTCGTTGAGGTCTGCAGGAAGAAATCGGCAAG
GCCAGCAGCGGGCGTGGAGATAACGGCATAGAGGATGCAAACGCTGTCAGGGGTTCAGCCT
CTCAGGGGCCCTGACTGAACCTTGGCAGAACAGACAGTCCCCCAGACCAGCCTCCCCCAGCT
TCTGCCGCTCCTCAGTGGGGAGGGAGAGCTCCAGTATGCATCCCTCAGCTTCCAGATGGT
GAAGCCTGGGACTCGCGGGGACAGGAGGCCACTGACACCGAGTACTCGGAGATCAAGATCC
ACAGA**TGA**GAAACTGCAGAGACTCACCTGATTGAGGGATCACAGCCCTCCAGGCAAGGGA
GAAGTCAGAGGCTGATTCTGTAGAATTAAACAGCCCTAACGTGATGAGCTATGATAACACT
ATGAATTATGTGCAGAGTGAAGAACACAGGCTTAGAGTCAAAGTATCTCAAACCTGAAT
CCACACTGTGCCCTCCCTTTATTTTTAACTAAAAGACAGACAAATTCTA



98/249

FIGURE 98

MLLPLLWGRERAEGQTSKLLTMQSSVTVQEGLCVHPCFSYPSHGWIYPGPVVHGYWF
REGANTDQDAPVATNNPARAVWEETRDRFHLLGDPHTKNTLSIRDARRSDAGRYFFRMEKG
SIKWNYKHHRLSVNVTALTHRPNILIPGTLESGCPQNLTCSPWACEQGTPPMISWIGTSVS
PLDPSTTRSSVLTLIPQPQDHGTSLTCQVTFPGASVTTNKTVHLNVSYPPQNLMTVFQGDG
TVSTVLNGSSLSLPEGQLRLVCAVDADSNPPARLSLSWRGLTLCPSQPSNPGVLELPWV
HLRDAAEFTCRAQNPLGSQQVYLNVLQSKATSGVTQGVVGAGATALVFLSFCVIFVVVR
CRKKSSARPAAGVGDTGIEDANAVRG SASQGPLTEPWAEDSPPDQPPPASARSSVGE
SLSFQMVKPWDSRGQEATDTEYSEIKIHR

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 351-370



99/249

FIGURE 99

GACGCCAGTGACCTGCCGAGGTGGCAGCACAGAGCTCTGGAG**ATGA**AGACCCTGTTCTGGTCA
GGTGCAGCTCGGCCTGGCGCTGCCCTGTCCTCACCTGGAGGGAGGATATCACAGG
GACCTGGTACGTGAAGGCCATGGTGGTCATAAGGACTTCCGGAGGACAGGAGGCCAGGA
AGGTGTCCCCAGTGAAGGTGACAGCCCTGGCGGTGGAAAGTTGGAAGGCCACGTTCACCTTC
ATGAGGGAGGATCGGTGCATCCAGAAGAAAATCCTGATGCGGAAGACGGAGGAGCCTGGCAA
ATACAGCGCCTATGGGGCAGGAAGCTCATGTACCTGCAGGAGCTGCCAGGAGGGACCACT
ACATCTTTACTGCAAAGACCAGCACCATGGGGCTGCTCCACATGGAAAGCTTGTGGGT
AGGAATTCTGATACCAACCAGGAGGCCCTGGAAGAATTAAAGAAATTGGTGCGCGCAAGGG
ACTCTCGAGGAGGACATTTCACGCCCTGCAGACGGGAAGCTGCGTCCCACAC**TAGG**
CAGCCCCCGGGTCTGCACCTCCAGAGGCCACCTTACCAACAGACAGGCCGGACCACCT
GGACCTACCCCTCCAGCCATGACCCCTCCCTGCTCCCACCCACCTGACTCCAAATAAGTCCT
TTTCCCCAAA



100/249

FIGURE 100

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65404
<subunit 1 of 1, 170 aa, 1 stop
<MW: 19457, pi: 9.10, NX(S/T): 0
MKTLFLGVTLGLAAALSFTLEEEDITGTWYVKAMVVDKDFPEDRRPRKVSPVKVTALGGGKL
EATFTFMREDRCIQKKILMRKTEEPGKYSAYGGRKLMYLQELPRRDHYIFYCKDQHHGGLLH
MGKLVGRNSDTNREALEEFKKLVQRKGLSEEDIFTPLQTGSCVPEH
```

Important features:

Signal peptide:

amino acids 1-17



101/249

FIGURE 101

GTTCCGCAGATGCAGAGGTTGAGGTGGCTGCGGGACTGGAAGTCATCGGGCAGAGGTCTCAC
AGCAGCCAAGGAACCTGGGGCCCGCTCCTCCCCCTCCAGGCC **ATG**AGGATTCTGCAGTTAA
TCCTGCTTGCTCTGGCAACAGGGCTTGTAGGGGGAGAGACCAGGATCATCAAGGGGTTCGAG
TGCAAGCCTCACTCCCAGCCCTGGCAGGCAGCCCTGTTGAGAAGACGCCGACTCTGTGG
GGCGACGCTCATGCCCGAGATGGCTCCTGACAGCAGCCACTGCCTCAAGCCCCGCTACA
TAGTTCACCTGGGGCAGCACAAACCTCCAGAAGGAGGGCTGTGAGCAGACCCGGACAGCC
ACTGAGTCCTTCCCCACCCCGGCTCAACAAACAGCCTCCCCAACAAAGACCACCGCAATGA
CATCATGCTGGTGAAGATGGCATGCCAGTCTCCATCACCTGGCTGTGCGACCCCTCACCC
TCTCCTCACGCTGTGTCAGTGCCTGCACAGCTGCCTCATTCGGCTGGGGCAGCACGTCC
AGCCCCCAGTTACGCCTGCCTCACACCTTGCATGCACATCACCATCATGAGCACCA
GAAGTGTGAGAACGCCTACCCCGAACATCACAGACACCATGGTGTGAGCAGCGTGCAGG
AAGGGGGCAAGGACTCCTGCCAGGGTGAECTCCGGGGCCCTCTGGTCTGTAACCAGTCTCTT
CAAGGCATTATCTCCTGGGGCCAGGATCCGTGTGCGATCACCCGAAAGCCTGGTGTACAC
GAAAGTCTGCAAATATGTGGACTGGATCCAGGAGACGATGAAGAACAAATT**TAG**ACTGGACCCA
CCCACCAAGCCATCACCCCTCCATTCCACTTGGTGTGGCTCTGTTACTCTGTTAAT
AAGAAACCTAAGCCAAGACCCCTACGAACATTCTTGGCCTCTGGACTACAGGAGATG
CTGTCACTTAATAATCAACCTGGGTTGAAATCAGTGAGACCTGGATTCAAATTCTGCCCTT
GAAATATTGTGACTCTGGGAATGACAACACCTGGTTCTGTTGATCCCCAGCCCCA
AAGACAGCTCCTGCCATATATCAAGGTTCAATAAATATTGCTAAATGAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAA



SEARCHED AND SERIALIZED
DEPT OF COMMERCE
U.S. PATENT & TRADEMARK OFFICE

102/249

FIGURE 102

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65405
<subunit 1 of 1, 250 aa, 1 stop
<MW: 27466, pI: 8.87, NX(S/T): 4
MRILQLILLALATGLVGETRIIKGFECKPHSQPWQAALFEKTRLLCGATLIAPRWLLTAAH
CLKPRYIVHLGQHNLQKEEGCEQRTTATESFPHPGFNNSLPNKDHRNDIMLVKMASPVSITW
AVRPLTLSSRCVTAGTSCLISGWGSTSSPQLRLPHTLRCANITIIIEHQKCENAYPGNITDTM
VCASVQEGGKDSCQGDGGPLVCNQSLQGIISWGQDPCAITRKPGVYTKVCKYVDWIQETMKNN
```

Important features:

Signal peptide:

amino acids 1-18

Serine proteases, trypsin family, histidine active site.

amino acids 58-63

N-glycosylation sites.

amino acids 99-102, 165-168, 181-184, 210-213

Glycosaminoglycan attachment site.

amino acids 145-148

Kringle domain proteins.

amino acids 197-209, 47-64

Serine proteases, trypsin family, histidine protein

amino acids 199-209, 47-63, 220-243

Apple domain proteins

amino acids 222-249, 189-222



103/249

FIGURE 103

GAGCAGTGTCTGGAGCCG**ATG**CCAAAAACCATGCATTCTTATTCA
GATTGTTCTGTGGGCCTTTACTGCTCAGAGACAAAAGAAAGAGGAGAGCACCGAAGAA
GTGAAAATAGAAGTTGCATCGTCCAGAAA**ACTG**CTAAGACAAGCAAGAAGGGAGACCT
ACTAAATGCCATTATGACGGCTACCTGGCTAAAGACGGCTCGAAATTCTACTGCAGCCGGA
CACAAAATGAAGGCCACCCCAAATGGTTGTTCTGGTGTGGCAAGTCATAAAAGGCCTA
GACATTGCTATGACAGATATGTGCCCTGGAGAAAAGCGAAAAGTAGTTATA
ACCCCCTTCATTGTCATAACGGAAAGGAAGGCATATGCAGAACGGCAAGATT
CCACGGATGCTACATTGATTGAGACATTAAACAAATAGAC
ATGGACAATGACAGGCAGCTCTAAAGCCGAGATAAACCTCTACTTGCAAAGGGATT
GAAGATGAGAAGCCACGTGACAAGTCATATCAGGATGCAGTTTAGAAGATATTTAAGA
AGAATGACCATTGATGGTGTGGCTTCATTCTCCAAGGAATACAATGTATA
ACCAACACGATGAAC**TAG**CATATTGTATTCTACTTTTTTTAGCTATTACTGTACTTATGTATA
AAACAAAGTCACTTTCTCCAAGTTGTATTGCTATTCCCTATGAGAAGATATTTGA
TCTCCCCAATACATTGATTGGTATAATAATGTGAGGCTGTTGCAAAC
TTAAAAAAAAAAAAA
AAAAA



104/249

FIGURE 104

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65406

<subunit 1 of 1, 222 aa, 1 stop

<MW: 25794, pI: 6.24, NX(S/T): 1

MPKTMHFLFRFIVFFYLWGLFTAQRQKKEESTEEVKIEVLHRPENCSKTSKKGDLLNAHYDG
YLAKDGSKFYCSRTQNEGHPKWFVLGVGQVIKGLDIAMTDMCPGEKRKVVIIPPSFAYGKEGY
AEGKIPPDATLIFEIELYAVTKGPRSIETFKQIDMDNDRQLSKAEINLYLQREFEKDEKPRD
KSYQDAVLEDIFKKNDHDGDGFISPKEYNVYQHDEL

Important features:

Endoplasmic reticulum targeting sequence.

amino acids 219-222

N-glycosylation site.

amino acids 45-48

FKBP-type peptidyl-prolyl cis-trans isomerase

amino acids 87-223, 129-142

EF-hand calcium-binding domain proteins

amino acids 202-214, 195-214



105/249

FIGURE 105

CAGAAATGCAGGGACCATTGCTTCTTCCAGGCCTCTGCTTCTGCTGAGCCTCTTGGAGCT
GTGACTCAGAAAACCAAAACTCCTGTGCTAAGTGCCCCCAAATGCTTCCTGTGTCAATAA
CACTCACTGCACCTGCAACCATGGATATACTTCTGGATCTGGCAGAAACTATTCACATTCC
CCTTGGAGACATGTAACGCCAGGCATGGTGGCTCGCGCCTGTAATCCCAGTTCTTGGGAAG
CCAAGGCAGGTGGATCACCTGAGGTCAAGGAGTTGAGACCAGCCTGGCCAACATAGTGAAAC
CCC GTGTCTACTAAAAATACAAAATCAGCCGGCGTGGTGGTCATGCCTGCAATCCCAGT
TACTCGGGAGGCTGAGGCAGGAGAACCGCTGAACACTCAGGAGGCAGAAGTTGCAGTGAACCC
AGATCCTGCCATTGCACTCCAGCATGGATGACAGAGCAAGACTCCGTCTAAAAAGAAAAGA
TAGTTCTTGTTCATTCGCGACTGCCCTCTCAGTGTTCCTGGATCCCCTCCAAATAA
AGTACTTATATTCTC



106/249

FIGURE 106

MQGPLLLPGLCFLLSLFGAVTQKTKTSCAKCPPNASCVNNTHCTCNHGYTSGSGQKLFTFPL
ETCNARHGGSR

Signal peptide:

amino acids 1-18



107/249

FIGURE 107

CAAGCAGGT CATCCCCTGGTGACCTCAAAGAGAAGCAGAGAGGGCAGAGGTGGGGGCAC
AGGGAAAGGGT GACCTCTGAGATTCCCCTTTCCCCAGACTTGGAAAGTGACCCACC**ATGG**
GGCTCAGCATCTTTGCTCCTGTGTGTTCTGGGCTCAGCCAGGCAGCCACACCGAAGATT
TTCAATGGCACTGAGTGTGGCGTAACTCACAGCCGTGGCAGGTGGGCTGTTGAGGGCAC
CAGCCTGCGCTGCGGGGGTGCCTTATTGACCACAGGTGGGCTCACAGCGGCTCACTGCA
CGGGCAGCAGGTACTGGGTGCGCCTGGGGAACACACGCCTCAGCCAGCTGACTGGACCGAG
CAGATCCGGCACAGCGGCTCTGTGACCCATCCGGTACCTGGGAGCCTGACGAGCCA
CGAGCACGACCTCCGGCTGCTGCGGCTGCGCCTGCCGTCCCGTAACCAGCAGCGTTCAAC
CCCTGCCCTGCCAATGACTGTGCAACCGCTGGCACCAGTGCCACGTCTCAGGCTGGGC
ATCACCAACCACCCACGGAACCCATTCCCGATCTGCTCCAGTGCCCTCAACCTCTCCATCGT
CTCCCATGCCACCTGCCATGGTGTGTATCCGGAGAACATCGAGCAACATGGTGTGTGCAG
GCGCGTCCGGGGCAGGATGCCCTGCCAGGGTGATTCTGGGGCCCTGTGGACAAGATGGCATCCCTGG
AGTCTACACCTATATTGCAAGTATGTGGACTGGATCCGGATGATCATGAGGAACA**TGAC**
CTGTTCCCTCCACCTCCACCCCCACCCCTTAACCTGGGTACCCCTCTGCCCTCAGAGCACC
AATATCTCCTCCATCACTCCCTAGCTCCACTCTGTGTTGCCCTGGAAACTCTTGGAAACTT
TAACTCCTGCCAGCCCTTAAGACCCACGAGCGGGTGAGAGAAGTGTGCAATAGTCTGGA
ATAAAATATAATGAAGGAGGGCAAAAAAAA



108/249

FIGURE 108

MGLSIFLLLCVLGLSQATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAH
CSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLRLPVRTSSV
QPLPLPNDCATAGTECHVSGWGITHPRNPFPDLLQCLNLSIVSHATCHGVYPGRITSNMVC
AGGVPGQDACQGDSGGPLVCGGVLQGLVSWGSVGPGCGQDGIPGVYTYICKYVDWIRMIMRNN

Signal peptide:

amino acids 1-17



109/249

FIGURE 109

GCGGCCACACG CAGCTAGCCGGAGCCCGGACCAGGCCCTGTGCCTCCTCGTCCCTCGC
CGCGTCCCGAAGCCTGGAGCCGGGGAGCCCCGCGCTGCCATGTCGGGCGAGCTCAGCA
ACAGGTTCCAAGGAGGGAAAGCGTTGGCTGCTCAAAGCCGGCAGGAGAGGAGGCTGGCC
GAGATCAACCGGGAGTTCTGTGACCAGAAGTACAGTGATGAAGAGAACCTCCAGAAAA
GCTCACAGCCTCAAAGAGAAGTACATGGAGTTGACCTGAACAATGAAGGCAGATTGACC
TGATGTCTTAAAGAGGATGATGGAGAAGCTTGGTGTCCCCAAGACCCACCTGGAGATGAAG
AAGATGATCTCAGAGGTGACAGGAGGGTCAGTGACACTATATCCTACCGAGACTTGTGAA
CATGATGCTGGGAAACGGTCGGCTGTCCTCAAGTTAGTCATGATGTTGAAGGAAAAGCCA
ACGAGAGCAGCCCCAAGCCAGTTGGCCCCCTCCAGAGAGAGACATTGCTAGCCTGCCTGA
GGACCCCGCCTGGACTCCCCAGCCTCCCACCCATACCTCCCTCCGATCTGCTGCCCTT
CTTGACACACTGTGATCTCTCTCTCATTTGTTGGTCATTGAGGGTTGTTGTGTT
TCATCAATGTCTTGTAAAGCACAAATTATCTGCCTTAAAGGGCTCTGGTCGGGAATCC
TGAGCCTGGGTCCCTCCCTCTCTTCTCCCTCCCTCCGCTCCGTGCAGAAGGGCTG
ATATCAAACCAAAACTAGAGGGGCAGGGCAGGGCAGGGAGGCTCCAGCCTGTGTTCCC
CTCACTTGGAGGAACCAGCACTCTCCATCCTTCAGAAAGTCTCCAAGCCAAGTTCAGGCTC
ACTGACCTGGCTCTGACGAGGACCCAGGCCACTCTGAGAAGACCTGGAGTAGGGACAAGG
CTGCAGGGCCTTTGGTTCCCTGGACAGTGCCTGGTCCAGTGCTCTGGTCACCC
AGGACACAGCCACTCGGGCCCCGCTGCCAGCTGATCCCCACTCATTCCACACCTTTCT
CATCCTCAGTGTGAAGGTGGAAAGGAAGGAGCTTGGCATTGGAGGCCCTCAAGAAGG
TACCAGAAGGAACCCCTCCAGTCCTGCTCTGCCACACCTGTGCAGGCAGCTGAGAGGCAG
CGTGCAGCCCTACTGTCCCTACTGGGGCAGCAGAGGGCTCGGAGGCAGAAGTGAGGCCTG
GGGTTGGGGAAAGGTAGTCAGTCAGTGCTGTTCCACCTTGTAGGGAGGAGACTGAGGGAC
CAGGATGGGAGAATGAGGAGTAAATGCTCACGGCAAAGTCAGCAGCACTGGTAAGCCAAGA
CTGAGAAATACAAGGTTGCTGTGACCCCAATCTGCTGAAAAAAAAAAAAAA



110/249

FIGURE 110

MSGELSNRFQGGKAFGLLKARQERRLAEINREFLCDQKYSDEENLPEKLTAFKYMEFDLN
NEGEIDLMSLKRMMEKLGVPKTHLEMKKMISEVTGGVSDTISYRDFVNMMLGKRSAVLKVM
MFEKGKANESSPKPVGPPPEDIASLP



111/249

FIGURE 111A

CGCGCTCCCCGCGCCTCCTGGGCTCCACCGTCTGCCCGCAGAGGCAGCCTCCTCCA
GGAGCGGGGCCCTGCACACC**ATG**CCCCCGGGTGGCAGGGTGGCGCCGCGCC
CGCCTGGCGCTGGCCTGGCGCTGGCGAGCGTCCTGAGTGGCCTCAGCGTCGCCTGCC
CACCAAGTGTACCTGCTCCGCTGCCAGCGTGGACTGCCACGGCTGGCCTCCCGCGGGTTC
CTCGGGCATCCCCGCAACGCTGAGCGCCTGACCTGGACAGAAATAATATCACCAGGATC
ACCAAGATGGACTTCGCTGGCTCAAGAACCTCCGAGTCTGCATCTGGAAGACAACCAGGT
CAGCGTCACTGAGAGAGGGCCTTCCAGGACCTGAAGCAGCTAGAGCGACTGCCCTGAACA
AGAATAAGCTGCAAGTCCTCCAGAATTGCTTTCCAGAGCACGCCAAGCTCACCAAGACTA
GATTGAGTGAACACAGATCCAGGGGATCCCAGGAAGGCCTCCGGCATCACCGATGT
GAAGAACCTGCAACTGGACAACAACCACATCAGCTGCATTGAAGATGGAGCCTCCGAGCGC
TGCGCATTGGAGATCCTAACACAACAACATCAGTCGATCCTGGTCACCAGC
TTCAACCACATGCCAAGATCCGAACTCTGCGCCTCACTCCAACCACCTACTGCGACTG
CCACCTGGCCTGGCTCTCGGATTGGCTGCAGCGACAGGACAGTTGCCAGTTCACACTCT
GCATGGCCTCTGTGCATTGAGGGCTTCAACGTGGCGATGTGCAGAAGAAGGAGTACGTG
TGCCCAGCCCCACTCGGAGCCCCATCCTGAATGCCAACTCCATCTCCTGCCCTCGCC
CTGCACGTGCAGCAAATAACATCGTGGACTGTGAGGAAAGGGCTTGATGGAGATTCTGCCA
ACTTGCCGGAGGGCATCGTCAAATACGCCAGAACAGAACTCCATCAAAGCCATCCCTGCA
GGAGCCTCACCCAGTACAAGAAACTGAAGCGAATAGACATCAGCAAGAACATCAGATATCGGA
TATTGCTCCAGATGCCTCCAGGGCTGAAATCACTCACATCGTGGCCTGTATGGGAACA
AGATCACCAGAGATTGCCAAGGGACTGTTGATGGCTGGTCTCCCTACAGCTGCTCCTCCTC
AATGCCAACAAAGATCAACTGCCTGCCGTGAAACACGTTCAGGACCTGCAGAACCTCAACTT
GCTCTCCCTGTATGACAACAAGCTGCAGACCATCAGCAAGGGCTTCGCCCTCTGCA
CCATCCAGACACTCCACTTAGCCAAAACCCATTGTGTGCAGTGCCTTAAGTGGCTG
GCCGACTACCTCCAGGACAACCCCATCGAGACAAGCGGGCCGCTGCAGCAGCCCG
ACTGCCAACAAAGCGATCAGCAGATCAAGAGCAAGAACAGTTCCGCTGCTCAGGCTCCGAGG
ATTACCGCAGCAGGTTCAGCAGCGAGTGCCTCATGGACCTCGTGTGCCAGGAGAAGTGTG
TGTGAGGGCAGATTGTGGACTGCTCAACCAGAACAGTGGTCCGCATCCCAAGCCACCTCCC
TGAATATGTCACCGACCTGCGACTGAATGACAATGAGGTATCTGTTCTGGAGGCCACTGGCA
TCTTCAAGAAGTTGCCAACCTGCCAAAATAATCTGAGTAACAATAAGATCAAGGAGGTG
CGAGAGGGAGCTTCGATGGAGCAGCCAGCGTGCAGGAGCTGATGCTGACAGGAAACCAGCT
GGAGACCGTGCACGGCGCGTGTCCGTTCCGCTCAGTGGCCTCAAAACCTTGATGCTGAGGA
GTAACTTGATCAGCTGTGTGAGTAATGACACCTTGCCGGCTGAGTCGGTGAGACTGCTG
TCCCTCTATGACAATCGGATCACCACCATCACCCTGGGCCCTCACACGCTGTCTCCCT
GTCCACCATAAACCTCCTGCTCAACCCCTCACTGCAACTGCCACCTGGCTGGCTCGGCA
AGTGGTTGAGGAAGAGGCAGTGTGAGTCAAGGACCTAGGTGCCAGAACCCATTTCCTC
AAGGAGATTCCCACAGGATGTGCCATCAGGACTTCACCTGTGATGGCAACGAGGAGAG
TAGCTGCCAGCTGAGCCCGCTGCCGGAGCAGTGCACCTGTATGGAGACAGTGGTGC
GCAGCAACAAGGGCTCCGCCCTCCCCAGAGGCATGCCAAGGATGTGACCGAGCTGTAC
CTGGAAGGAAACCACCTAACAGCCGTGCCAGAGAGCTGTCGCCCTCCGACACCTGACGCT
TATTGACCTGAGCAACAACAGCATCAGCATGCTGACCAATTACACCTCAGTAACATGTCTC
ACCTCTCCACTCTGATCCTGAGCTACAACCGGCTGAGGTGCATCCCCGTCCACGCCCTCAAC
GGGCTGCCGTCCCTGCGAGTGCTAACCCCTCATGGCAATGACATTTCAGCGTCTGAAGG
CTCCTCAACGACCTCACATCTTCCCACATCTGGCGCTGGGAACCAACCCACTCCACTGTG
ACTGCAGTCTCGGTGGCTGCGAGTGGTGAAGGGGGTACAAGGAGCCTGGCATCGCC
CGCTGCAGTAGCCCTGAGCCATGGCTGACAGGCTCTGCTCACCACCCAAACCCACCGCTT
CCAGTGCAAAGGGCAGTGGACATCAACATTGTGGCAAATGCAATGCCCTGCCAGCC
CGTGCAAGAATAACGGGACATGCACCCAGGACCCCTGTGGAGCTGTACCGCTGTGCCCTGCC



112/249

FIGURE 111B

TACAGCTACAAGGGCAAGGACTGCACTGTGCCCATCAACACCTGCATCCAGAACCCCTGTCA
GCATGGAGGCACCTGCCACCTGAGTGACAGGCCACAAGGATGGGTTAGCTGCTCCTGCCCTC
TGGGCTTGAGGGGCAGCGGTGTGAGATCAACCCAGATGACTGTGAGGACAACGACTGCGAA
AACAAATGCCACCTGCGTGGACGGGATCAACAACTACGTGTATCTGTCCGCCAACTACAC
AGGTGAGCTATGCGACGAGGTGATTGACCACTGTGTGCCTGAGCTGAACCTCTGTCAAGCATG
AGGCCAAGTGCATCCCCCTGGACAAAGGATTCAGCTGCGAGTGTGTCCCTGGCTACAGCGGG
AAGCTCTGTGAGACAGACAATGATGACTGTGTGGCCCACAAGTGCCGCCACGGGGCCAGTG
CGTGGACACAATCAAATGGCTACACATGCACCTGCCCTCAGGGCTTCAGTGGACCCCTCTGTG
AACACCCCCCACCACATGGTCTACTGCAGACCAGCCATGCACCAGTACGAGTGCCAGAAC
GGGGCCCAAGTGCATCGTGGTGCAGCAGGAGCCCACCTGCCGTGCCACCAGGCTCGCCGG
CCCCAGATGCGAGAAGCTCATCACTGTCAACTCGTGGGCAAAGACTCCTACGTGGAACCTGG
CCTCCGCCAAGGTCCGACCCCAGGCCAACATCTCCCTGCAGGTGGCCACTGACAAGGACAAC
GGCATCCTCTCTACAAAGGAGACAATGACCCCCCTGGCACTGGAGCTGTACCGAGGGCACGT
GGGGCTGGTCTATGACAGCCTGAGTTCCCCCTCCAACCACAGTGTACAGTGTGGAGACAGTGA
ATGATGGCAGTTCACAGTGTGGAGCTGGTGACGCTAAACCAGACCCCTGAACCTAGTAGTG
GACAAAGGAACCTCAAAGAGCCTGGGGAAAGCTCCAGAAGCAGCCAGCAGTGGCATCAACAG
CCCCCTCTACCTTGGAGGCATCCCCACCTCCACCGGCCTCTCCGCCTTGCAGGGCACGG
ACCAGGCCTCTAGGCGGCTCCACGGATGCATCCATGAGGTGCGCATCAACAAACGAGCTGCA
GACTTCAAGGCCCTCCCACCACAGTCCCTGGGGTGTCAACCAGGCTGCAAGTCCTGCACCGT
GTGCAAGCACGGCCTGTGCCGCTCCGTGGAGAAGGACAGCGTGGTGTGCGAGTGGCCAG
GCTGGACCAGGCCACTCTGCAGCACCAGGAGGGCCGGACCCCTGCCCTCGGCCACAGATGCCAC
CATGGAAAATGTGTGGCAACTGGGACCTCATACATGTGCAAGTGTGCCAGGGCTATGGAGG
GGACTTGTGTGACAACAAGAATGACTCTGCCAATGCCCTGCTCAGCCTCAAGTGTACCATG
GGCAGTGCCACATCTCAGACCAAGGGAGCCCTACTGCCCTGCCCCGGCTTAGCGGC
GAGCACTGCCAACAAAGAGAATCCGTGCCCTGGACAAGTAGTCCGAGAGGTGATCCGCC
GAAAGGTTATGCATCATGTGCCACAGCCTCCAAGGTGCCCATCATGGAATGTGTTGGGGCT
GTGGGCCCTAGTGTGCCAGCCCACCCGCAGCAAGCGGCCAGAAATACGTCTTCCAGTGCACG
GACGGCTCTCGTTGTAGAAGAGGTGGAGAGACACTTAGAGTGCAGCTGCCGTGTT
CTAAGCCCTGCCGCCCTGCCACCTCTGGACTCCAGCTTGTGATGGAGTTGGACAGCC
ATGTGGGACCCCCCTGGTGATTGACCATGAAGGAAATGAAGCTGGAGAGGAAGGTAAGAAGA
AGAGAATATTAAGTATATTGTAACAAAAAATAGAACTTAAAAAAAAAAAAAAA
AAAAAA



113/249

FIGURE 112

MAPGWAGVGA AVR LAL ALA SVLS GPP AVAC PT KCT CSA ASVD CHGL GLRA VPRG I PRN
AERLD LDR NNITR ITKMD FAGL KNL RVL HLED NQSVI ERGA F QDL KQL ER LRL NKN KLQVL
PELL F QST PKL TRLD LSEN QI OGIP RKA FRG IT DV KNL QL DNNH IS CIED GA FR AL RD LEIL
TLNNNN IS RIL VTS FN HMP KIR TL RL HS NH LY CD CH LA WL SD WLR QR RT VG QFT LC MAP VHL
RGF NVAD VQ KKEY VC PAP HSE PP SC NANSIS CP SP CT CS NNIV DC RG KGL MEIP AN LPEG IV
EIR LEQ NSI KA IPAG AFT QY KKL KRI DISK NQ IS DI APDA F QGL KSL TSL VLY GN KITE IA K
GL FD GL VSL QL L L NANK IN CL RV NT F QDL QLN NL LS LY DN KLT IS KGL FA PL QSI QT LHL
AQNP FV CD CH LKWL ADYL QDN PIET SGAR C S P RRL AN KRI S QIK SKK FRC SG S E DYRS RFS
SEC FMD LV CPE KCR CEGT IV DC SNQ KLV RI PSHL PEY VT DL RL ND NEV SLE AT G IF KK LPN
LR KIN L SNN KI KE VREG AFD GA ASV QEL M LT G NQ LET VH GRV FR GL SG LK TLM RSN L I S CV
SND TFA GL SS VR LL S LY DN RITT IT P G AFT TL VSL STIN LL S NP FNC NC HLA WL GK WLR KRR
IV SGN PRC QK PFF LKE IPI QD VAI QD FT CD GNE ESSC QLS PRC PE QCT CMET VV RC SN KGL R
AL PR GM PKD VTE LY LEG NHT AV PREL SAL RHL TL ID LS NN SIS M LT NY TFS NM SHL ST LIL
SY N RL RCI PV HAF NGL RSL RV L TL HG ND ISSV PEG SF ND LT SL SH L AL GTN PL HC DC S LR WL
SEW V KAG YKE PG I ARCS S PEP M DR LL TT PTH RF QCK GPV D IN I VAK CNA CL S PCK NNG T
CT QDP VELY RYCA CP SYKG KDC TVP INT CI QN PC QH GT CHL SD SH KDG FSC S C PLG FEG QR
CE I NPD DC ED ND CENN AT CVD GIN NYVC IC CPP NYT GEL CDE VID HCV PEL NLC QHE AKC I PL
DK GFS CEC VP GY SG KLC ET DND DC VA HK CRH GA QC VDT ING YT CT CP QG FSG P FCE H PPP MV
LL QTP C DQ YEC QNG AQC IV VQ QEP TC RC PPG FAG PR CE K L IT VNF VG KDS Y VEL AS A KV RP
QAN ISL QV AT DK DNG ILL Y KG DND PL A LE LY QGH VRL VY DS LSS PTT VY SVE T VND QF HS
VEL VTL NQ TL NL VV DK GTP KSL GKL QP AVG IN S PLY LG GI PT ST GLS AL RQ GT DR PL GG F
HG CI HE VR INN EL QDF KAL PP QSL GVP GCK S CT VCK HGL CRS VE KDS VV C E RPG WT G PLC
DQE ARD PCL GH RCH HG KCV AT GT SYM CK CA EG YGG D L C DN K N DS AN AC SA FK CH H G Q CH IS D
QGE PYC IL C QPG FSG E HC Q QEN PCL GQ VV RE VIR RQ KG YAS CAT ASK V PIM E CRGG CGP QCC Q
PTR SK RR KYV F QCT DG SS F VEE EVER H LEC G CL ACS

Signal peptide:

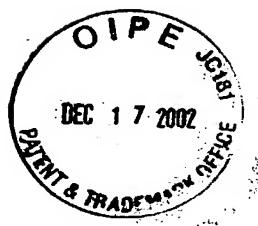
amino acids 1-27



114/249

FIGURE 113

GGATGCAGGACGCTCCCTGAGCTGCCTGTACCGACTAGGTGGAGCAGTGTTCCTCCGCA
GAECTCAACTGAGAAGTCAGCCTCTGGGGCAGGCACCAGGAATCTGCCTTTCAGTTCTGTCT
CCGGCAGGCTTGAGGATGAAGGCTGCCATTCTGACCCCTATTGGCTGCCTGGTACAG
GCGCCGAGTCCAAAATCTACACTCGTTGCAAACCTGGCAAAATATTCTCGAGGGCTGCCCTG
GACAATTACTGGGGCTTCAGCCTGGAAACTGGATCTGCATGGCATATTATGAGAGCGGCTA
CAACACCACAGCCCCGACGGCCTGGATGACGGCAGCAGTGCAGTGCATCTCCAGATCA
ACAGCTCGCGTGGTGCAGACGCGAAAGCTGAAGGAGAACACCAGTGCATGTCGCCTGC
TCAGCCTTGATCACTGATGACCTCACAGATGCAATTATCTGTGCCAGGAAAATTGTTAAAGA
GACACAAGGAATGAACATTGGCAAGGCTGGAAGAACATTGTGAGGGCAGAGACCTGTCCG
AGTGGAAAAAAGGCTGTGAGGTTCCTAAACTGGAACGGACCCAGGATGCTTGCAGCAAC
GCCCTAGGATTTGCAGTGAATGTCAAATGCCGTGTCATCTGTCCCCTTCCCAATA
TTCCTTCTCAAACCTGGAGAGGGAAAATTAGCTATACTTTAAGAAAATAATTTCCAT
TTAAATGTC



DEC 17 2002

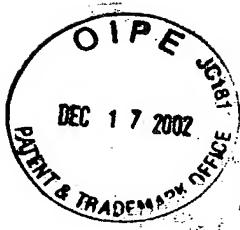
115/249

FIGURE 114

MKAAGILTLIGCLVTGAESKIYTRCKLAKIFSRAGLDNYWGFSLGNWICMAYYESGYNTTAP
TVLDDGSIDYGIFQINSFAWCRRGKLKENNHCHVACSLITDDLTDAAIICARKIVKETQGMN
YWQGWKKHCEGRDLSEWKKGCEVS

Signal peptide:

amino acids 1-19



116/249

FIGURE 115

CAGGCCATTGCATCCCACTGTCCTGTGTTGGAGCCAGGCCACACCGTCTCAGCAGTGT
CATGTGTTAAAAACGCCAAGCTGAATATATC**ATG**CCCCTATTAAAACTTGTACATGGCTCCC
CATTGGTTTGAGAAAAGTTCAAGCTTTACCTGGTCTGCCTGTATCCCAGTGTTC
AGGCTGGCTAGACGGCGGAAGAAGATCCTATTTACTGTCACCTCCCAGATCTGCTTCTCAC
CAAGAGAGATTCTTCTTAAACGACTATAACAGGGCCCCAATTGACTGGATAGAGGAATACA
CCACAGGCATGGCAGACTGCATCTAGTCACACAGCCAGTTCACAGCTGCTGTTAAGGAA
ACATTCAAGTCCCTGTCTCACATAGACCCCTGATGTCCTCTATCCATCTCAAATGTCACCAG
CTTGACTCAGTTGTCCTGAAAAGCTGGATGACCTAGTCCCAAGGGGAAAAATTCTGC
TGCTCTCCATCAACAGATAcgaaAGGAAGAAAATCTGACTTGGACTGGAAGCCCTAGTA
CAGCTGCGTGGAAAGATTGACATCCAAGATTGGGAGAGGGTCATCTGATCGTGGCAGGTGG
TTATGACGAGAGAGTCCTGGAGAATGTGGAACATTATCAGGAATTGAAGAAAATGGTCAAAC
AGTCCGACCTTGGCCAGTATGTGACCTTCTGAGGTCTTCAGACAAAACAGAAAATCTCC
CTCCTCCACAGCTGCACGTGTGCTTACACACCAAGCAATGAGCATTGGCATTGTCCC
TCTGGAAGCCATGTACATGCAGTGCCAGTCATTGCTGTTAATTGGGTGGACCCTGGAGT
CCATTGACCACAGTGTACAGGGTTCTGTGTGAGCCTGACCCGGTGCACCTCTCAGAAGCA
ATAGAAAAGTTATCCGTGAACCTTCTTAAAGCCACCATGGGCCTGGCTGGAAGAGCCAG
AGTGAAGGAAAAATTTCCTGAAGCATTACAGAACAGCTCTACCGATATGTTACCAAAC
TGCTGGT**TAA**TCAGATTGTTTAAGATCTCCATTAATGTCATTGTTATGGATTGTAGACC
CAGTTTGAAACCAAAAAAGAAACCTAGAACATCTAATGCAAGAGAGATTTAAAAATAAA
CTTGAGTCTGAATGTGAGCCACTTCCTATATACCACACCTCCGTCCACTTTCAGAAA
AACCATGTCTTATGCTATAATCATTCAAATTGCCCAGTGTAAAGTTACAAATGTGGTG
TCATTCCATGTTCAAGCAGAGTATTAAATTATATTCTGGGATTATTGCTCTGTCTA
TAAATTGAAATGATACTGTCCTTAATTGGTTTCATAGTTAAGTGTATCATTCAA
AGTTGATTAATTGGCTTCAGTATAATGAGAGCAGGGCTATTGAGTTCCAGATTCAA
CCACCGAAGTGTCACTGTCATCTGTTAGGAAATTGTTGTCCTGTCTTGCCTGGATC
CATAGCGAGAGTGCTCTGTATTGTTAAGATAATTGTTAGGACACTGAGATATAA
TAAAAGGTGTTATCATAAAAAAAAAAAAAAA



117/249

FIGURE 116

MPLLKLVHGSPLVFGEKFKLFTLVSACIPVFRALARRKKILFYCHFPDLLLTKRDSFLKRLY
RAPIDWIEEYTTGMADCILVNSQFTAASFKETFKSLSHIDPDVLYPSLNVTSFDSVVPEKLD
DLVPKGKKFLLLSINRYERKKNLTLALEALVQLRGRLTSQDWERVHLIVAGGYDERVLENVE
HYQELKKMVQQSDLGQYVTFLRSFSDKQKISLLHSCTCVLYTPSNEHFGIVPLEAMYMQCPV
IAVNSGGPLESIDHSVTGFLCEPDPVHFSEAIKEKFIRESLKATMGLAGRARVKEKFSPEAF
TEQLYRYVTKLLV

Signal peptide:

amino acids 1-15



118/249

FIGURE 117

GAATACGCCGATCCGAGACGTGGCTCCCTGGCGGCAGAACCATGTTGGACTTCGCGATCTT
CGCCGTTACCTTCTTGCTGGCGTTGGTGGGAGCCGTGCTCACCTCTATCCGGCTTCCAGAC
AAGCTGCAGGAATTCCAGGGATTACTCCAAC TGAAAGAAAAAGATGGTAATCTTCCAGATATT
GTGAATAGTGGAAAGTTGCATGAGTCCTGGTTAATTGCATGAGAGATATGGCCTGTGGT
CTCCTCTGGTTGGCAGGCGCCTCGTGGTAGTTGGCACTGTTGATGTACTGAAGCAGC
ATATCAATCCCATAAGACATCGGACCCTTGAAACCATGCTGAAGTCATTATTAAGGTAT
CAATCTGGTGGTGGCAGTGTGAGTGAAAACACATGAGGAAAAAATTGTATGAAAATGGTGT
GAATGATTCTCTGAAGAGTAAC TTGCCCTCCTCAAAGCTTCAGAAGAATTATTAGATA
AATGGCTCTCCTACCCAGAGACCCAGCACGTGCCCTCAGCCAGCATATGCTGGTTGCT
ATGAAGTCTGTTACACAGATGGTAATGGTAGTACATTGAAGATGATCAGGAAGTCATTG
CTTCCAGAAGAACATGGCACAGTTGGCTGAGATTGGAAAAGGCTTCTAGATGGTCAC
TTGATAAAAACATGACTCGGAAAAACAATATGAAGATGCCCTCATGCAACTGGAGTCTGTT
TTAAGGAACATCATAAAAGAACGAAAAGGAAGGAACCTCAGTCAACATATTTCATTGACTC
CTTAGTACAAGGAAACCTTAATGACCAACAGATCCTAGAAGACAGTATGATATTTCTCTGG
CCAGTTGCATAATAACTGCAAAATTGTGTACCTGGCAATCTGTTTTAACCACCTCTGAA
GAAGTTCAAAAAAAATTATATGAAGAGATAAACCAAGTTGGAAATGGCCTGTTACTCC
AGAGAAAATTGAGCAGCTCAGATATTGTCAGCATGTGCTTGTGAAACTGTTGAACTGCCA
AACTGACTCCAGTTCTGCCAGCTCAAGATATTGAAGGAAAATTGACCGATTATTATT
CCTAGAGAGACCCCTCGTCCTTATGCCCTGGTGTGGTACTTCAGGATCCTAAACTTGGCC
ATCTCCACACAAGTTGATCCAGATCGGTTGATGAATTAGTAATGAAAACCTTCC
CACTTGGATTCTCAGGCACACAGGAGTGTCCAGAGTTGAGGTTGCATATATGGGACACCACA
GTACTTCTTAGTGTATTGGTAAGAGACTGCACCTACTTCTGTGGAGGGACAGGTTATTGA
AACAAAGTATGAACTGGTAACATCATCAAGGGAAGAAGCTGGATCACTGTCTCAAAGAGAT
ATTAAATTTATACATTAAAATCATTGTTAAATTGATTGAGGAAAACAACCATTAAAAA
AAATCTATGTTGAATCCTTTATAAACCAAGTATCAGTACTTGTAAATATAAACACCTATTGTAC
TTAA



119/249

FIGURE 118

MLDFAIFAVTFLLALVGAVLYLYPASRQAAGIPGITPTEEKDGNLPDIVNSGSLHEFLVNLH
ERYGPVVSFWFGRRLVVSLGTVDVLKQHINPNKTSDPFETMLKSLLRYQSGGGSVSENHMRK
KLYENGVTDSLKSNFALLKLSEELLDKWLSYPETQHVPLSQHMLGFAMKSVTQMVMGSTFE
DDQE VIRFQKNHGTWSEIGKGFLDGSLDKNMTRKKQYEDALMQLESVRNIIKERKGRNFS
QHIFIDSLVQGNLNDQQILEDSMIFSLASCIITAKLCTWAICFLTTSEEVQKKLYEEINQVF
GNGPVTPEKIEQLRYCQHVL CETVRTAKLTPVSAQLQDIEGKIDRFIIPRETLVLYALGVVL
QDPNTWPSPHKFDPDRFDDELVMKT FSSLGFSGTQECPELRFAYMVT VLLSVLVKRLHLLS
VEGQVIETKYELVTSSREEAWITVSKRY

Signal peptide:

amino acids 1-18

Transmembrane domain:

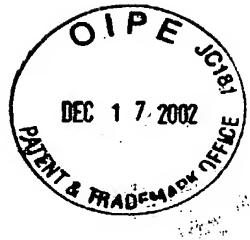
amino acids 271-290



120/249

FIGURE 119

CTAGATTGTCGGCTTGCAGGGAGACTCAGGAGTCGCTGTCTCTGAACCTCCAGCCTCAGA
GACCGCCGCCCTGTCCCCGAGGGCC**AT**GGGCCGGTCTCAGGGCTTGTGCCCTCGCTTC
CTGACGCTCCTGGCGCATCTGGTGGTCGTACACCTTATTCTGGTCCCAGGACAGAACAT
ACAGGCCTGCCTGCCTCTCACGTTACCCCCGAGGAGTATGACAAGCAGGACATTCACTGG
TGGCCGCCTCTGTACCCCTGGCCTCTTGCACTGGAGCTGGCCGGTTCCCTCAGGA
GTCTCCATGTTAACAGCACCCAGAGCCTCATCTCCATTGGGCTCACTGTAGTGCATCCGT
GGCCCTGTCCCTTCTCATATTGAGCGTTGGAGTGCACACTACGTATTGGTACATTTGTCT
TCTGCAGTGCCTTCCAGCTGTCACTGAAATGGCTTATTGTCACCGTCTTGGCTGAAA
AAGAAACCCCTTC**TG**ATTACCTTCATGACGGAACCTAACGGACGAAGCCTACAGGGCAAGGG
CCGCTTCGTATTCTGGAAGAAGGAAGGCATAGGCTTCGGTTTCCCTCGGAAACTGCTTC
TGCTGGAGGATATGTGTTGGAATAATTACGTCTGAGTCTGGGATTATCCGCATTGTATTTA
GTGCTTTGTAATAAAATATGTTTAGTAACATTAAAGACTTATACAGTTAGGGACA
ATTAAAAAAAAAAAAA



121/249

FIGURE 120

MGRVSGLVPSRFLTLLAHLVVVITLFWSRDSNIQACLPLTFTPEEYDKQDIQLVAALSVTLG
LFAVELAGFLSGVSMFNSTQSLISIGAHCSASVALSFFIFERWECTTYWYIFVFCSALPAVT
EMALFVTVFGLKKP

Transmembrane domain:

amino acids 12-28 (type II), 51-66, 107-124



U. S. PATENT AND TRADEMARK OFFICE
SEARCHED SERIALIZED INDEXED
RECEIVED DEPT. OF COMMERCE

122/249

FIGURE 121

TCCCGGACCTGCCGCCCTGCCACT**ATGT**CCCGCCGCTCTATGCTGCTTGCCTGGGCTCTCC
CCAGCCTCCTTCGACTCGGAGCGGCTCAGGAGACAGAAGACCCGGCCTGCTGCAGCCCCATA
GTGCCCCGGAACGAGTGGAAAGGCCCTGGCATCAGAGTGCGCCAGCACCTGAGCCTGCCCTT
ACGCTATGTGGTGGTATCGCACACGGCGGGCAGCAGCTGCAACACCCCCGCCTCGTGCCAGC
AGCAGGCCCGGAATGTGCAGCACTACCACATGAAGACACTGGGCTGGTGCACGTGGCTAC
AACTTCCTGATTGGAGAAGACGGGCTCGTATACGAGGGCCGTGGCTGGAACTTCACGGGTGC
CCACTCAGGTCACTTATGGAACCCATGTCCATTGGCATCAGCTTCATGGCAACTACATGG
ATCGGGTGCCAACCCCCAGGCCATCCGGGCAGCCCAGGGTCTACTGGCCTGCGGTGTGGCT
CAGGGAGCCCTGAGGTCCAACATATGTGCTCAAAGGACACCAGGATGTGCAGCGTACACTCTC
TCCAGGCAACCAGCTCTACCACCTCATCCAGAATTGGCACACTACCGCTCCCC**TGAGGCC**
CTGCTGATCCGCACCCATTCCCTCCCATGGCAAAAACCCCAGTGTCTCCTTCTCCA
ATAAAGATGTAGCTC



SEARCHED SERIALIZED INDEXED

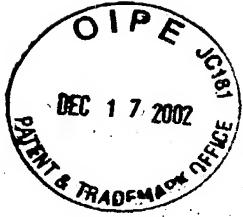
123/249

FIGURE 122

MSRRSMLLAWALPSLLRLGAAQETEDPACCSPIVPRNEWKALASECAQHLSLPLRYVVVSHT
AGSSCNTPASCQQQARNVQHYHMKTLCWCDVGYNFLIGEDGLVYEGRGWNFTGAHSGHLWNP
MSIGISFMGNYMDRVPTPQAIRAAQGLLACGVAQGALARSNYVLKGHRDVQRTLSPGNQLYHL
IQNWPHYRSP

Signal peptide:

amino acids 1-20



124/249

FIGURE 123

CTGGGACCCCGAAAAGAGAAGGGGAGAGCGAGGGGACGAGAGCGGAGGAAGATGCAACT
GACTCGCTGCTGTTCTGGTGCAGGGTAGCCTCTATCTGGTCATCTGTGGCCAGG
ATGATGGTCCTCCCGGCTCAGAGGACCCTGAGCGTGATGACCACGAGGGCCAGCCCCGGCC
CGGGTGCCTCGGAAGCGGGGCCACATCTCACCTAACGCTCCGCCCATGGCCAATTCCACTCT
CCTAGGGCTGCTGGCCCCGCCTGGGGAGGCTTGGGCATTCTTGGCAGCCCCCAACGCC
CGAACACAGCCCCCACCCCTCAGCCAAGGTGAAGAAAATCTTGGCTGGGCAGTCTAC
TCCAACATCAAGACGGTGGCCCTGAACCTGCTCGTCACAGGAAGATTGTGGACCATGGCAA
TGGGACCTTCAGCGTCCACTTCAAACACAATGCCACAGGCCAGGGAAACATCTCCATGCC
TCGTGCCCCCCAGTAAAGCTGTAGAGTCCACCAGGAACAGCAGATCTCATCGAACCCAAG
GCCTCCAAAATCTCAACTGCCGGATGGAGTGGAGAAGGTAGAACGGGCCGGACCTC
GCTTGACCCACGACCCAGCCAAGATCTGCTCCCAGACGCCAGCTCAGAGCTCAGCACCT
GGAGCTGCTCCCAGCCCTCAAAGTCGTCTGTCTACATGCCCTTACAGCACGGACTAT
CGGCTGGTCCAGAAGGTGTGCCAGATTACAACCTACCATAGTGAACCCCTACTACCCATC
TGGGTGACCCGGGGCAGGCCACAGAGGCCAGGGCTGGAGGACAGGCCTGCCATGC
AGGAGACCATCTGGACACCCGGCAGGGAAAGGGTTGGCCTCAGGCAGGGAGGGGGTGGAG
ACGAGGAGATGCCAAGTGGGCCAGGGCCAAGTCTCAAGTGGCAGAGAAAGGGTCCAAGTG
CTGGTCCCAACCTGAAGCTGTGGAGTGACTIONATCACAGGAGCACTGGAGGAGGAGTGGC
CTCTGTGCAGCCTCACAGGGCTTGCCACGGAGCCACAGAGAGATGCTGGGTCCCCGAGGCC
TGTGGCAGGCCGATCAGTGTGCCAGATCAAGTCATGGAGGAAGCTAACCCCTTGGTT
CTTGCCATCCTGAGGAAGATAGCAACAGGGAGGGGAGATTCACTCAGTGTGGACAGCCTG
TCAACTTAGGATGGATGGCTGAGAGGGCTTCCCTAGGAGCCAGTCAGCAGGGTGGGTGGGC
CAGAGGAGCTCCAGCCCTGCCTAGTGGGCCCTGAGCCCTTGTGCTGAGCATG
GCATGAGGCTGAAGTGGCAACCCCTGGGTCTTGATGTCTTGACAGATTGACCATCTGTCTC
CAGCCAGGCCACCCCTTCAAAATTCCCTTCTGCCAGTACTCCCCCTGTACCAACCCATT
GCTGATGGCACACCCATCCTAACGTAAGACAGGACGATTGTGGCTCCACACTAACGCC
ACAGCCCATCCCGGTGCTGTGTCCCTTCCACCCCAACCCCTGCTGGCTCCTCTGGAG
CATCCATGTCCCAGGAGAGGGTCCCTCAACAGTCAGCCTCACCTGTCAAGACCGGGTTCTCC
CGGATCTGGATGGCGCCGCCCTCTCAGCAGGGCACGGTGGGCGGGGCCGGCCAGA
GCATGTGCTGGATCTGTTCTGTGTCTGTGGTGGGGAGGGAGGGAAAGTCTTGT
GAAACCGCTGATTGCTGACTTTGTGTGAAGAATCGTGTCTGGAGCAGGAATAAGCTT
GCCCGGGCA



125/249

FIGURE 124

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66521
><subunit 1 of 1, 252 aa, 1 stop
><MW: 28127, pI: 8.91, NX(S/T): 5
MQLTRCCFVFLVQGSLYLVICQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPNSRPMAN
STLLGLLAPPGEAWGILGQPPNRPNHSPPSAKVKKIFGWGDFYSNIKTVANLLVTGKIVD
HGNGTFSVHFQHNATGQGNISISLVPPSKAVEFHQEQQIFIIEAKASKIFNCRMEWEKVERGR
RTSLCTHDPAKICSRDHAQSSATWSCSQPKVVCVYIAFYSTDYRLVQKVPDNYHSPTY
YPSG
```

Important features of the protein:

Signal peptide:

amino acids 1-14

N-glycosylation sites.

amino acids 62-65, 127-130, 137-140, 143-146

2-oxo acid dehydrogenases acyltransferase

amino acids 61-71



126/249

FIGURE 125

GTGAATGTGAGGGTTGATGACTTCAGATGTCTAGGAACCAGAGTGGGTGCAGGGGCCCA
GGCAGGGCTGATTCTGGCGGAGGAGAGTAGGGTAAAGGGTCTGCATGAGCTCCTTAAAG
GACAAAGGTAACAGAGCCAGCGAGAGAGCTCGAGGGAGACTTGAATTCAAGCCACAGAAT
TGGTGGAAAGTGTGCGCGCCGCCGCGCTCGCTCCTGCAGCGCTGTCGACCTAGCCGCTAG
CATCTTCCCAGCACCGGGATCCCGGGTAGGAGGCCACGCCGGCGAGCACCAGGCCAGCC
GGCTGCGGCTGCCACACGGCTCACCATGGGCTCCGGCGCCGGCGCTGTCGCCGGTGCCG
GCCGTGCTGCTGGCCTCACGCTGCCGGGCTGCCGTCTGGCACAGAACGACACGGAGCC
CATCGTGCTGGAGGGCAAGTGTCTGGTGGTGCAGCTCGAACCCGCCACGGACTCCAAGG
GCTCCTCTCCTCCCCGCTGGGATATCGGTCCGGCGGCCACTCCAAGGTGCGCCTCTCG
GCGGTGCGGAGCACCAACCACGAGCCATCCGAGATGAGCAACAAGACCGCATCTTACTT
CGATCAGATCCTGGTGAATGTGGTAATTTTACATTGGAGTCTGTCTTAGCACCAA
AAAAAGGAATTTACAGTTCAAGTTCACTGGGAAAGTCTACCAAGAGCCAAACTATCCAG
GTTAACTTGATGTTAAATGGAAAACCAGTAATATCTGCCTTGCAGGGACAAAGATGTTAC
TCGTGAAGCTGCCACGAATGGTGTCTGCTCACCTAGATAAAAGAGGATAAGGTTACCTAA
AACTGGAGAAAGGTAAATTGGTGGAGGCTGGCAGTATTCCACGTTCTGGCTTCTGGT
TTCCCCCTTAGGATTCAATTCTCCATGATGTTCATCCAGGTGAGGGATGACCCACTCCTG
AGTTATTGGAAGATCATTTCATCATTGGATTGATGTCTTTATTGGTTCTCATGGTG
GATATGGATTCTAAGGATTCTAGCCTGCTGAACCAATAAAATTCACAGATTATTGTG
TGTGTCTGTTCACTGTTGGATTGGACTCTAACGAGATAATACTATGCTTAAATGTA
ACAGTCAAAAGCTGCTGCAAGACTTATTCTGAATTCTGCTTGGGATTACTGAATTAGT
TACAGATGTGGAATTATTGTTAGTTAAAAGACTGGCAACCAGGTCTAAGGATTAGA
AAACTCTAAAGTTCTGACTTCAATCAACGGTAGTGTGATACTGCCAAAGAACTGTATACTG
TGTTAATATATTGATTATTTGTTTATTCTGGATTAGTTGTTGGTTCTGTAA
AAAACCTGGATTTTTTCACTGGATTATGTTCTCTTAAATAAGGTAATGAA
TGGCTTGCACAAATTACCTGACTACGATATCATCGACATGACTCTCTCAAAAAAAA
GAATGCTTCAAGTTGATTGTATTGATAATTGTATGTGAAAGAGTCATATTCCAAGTTATATT
TTCTAAGAAGAAGAATAGATCATAATCTGACAAGGAAAAGTTGCTTACCCAAATCTAAG
TGCTCAATCCCTGAGCCTCAGCAAAACAGCTCCCGAGGGAAATCTTACCTTATTGC
TCAACTTAAATTAAAATGATTGATAATAACCACCTTATTAAAAACCTAAGGTTTTTTT
TCCGTAGACATGACCACTTATTAAACTGGTGGGGATGCTGTTCTAATTACCTAT
TTTCAAGGCTTGTATTGAAGTATCATCTGGTTTGCCTTAACCTTAAATTGTA
TATATTATCTGTTAGCTAATATTAAATTCAAATATCCCATACTAAATTAGTGCATAT
CTTGTCTTTGTATAGGTCTATGAATTCAAAATTATTATGTCTGTTAGAATAAAGA
TTAATATATGTTAAAAAAA



127/249

FIGURE 126

MGSGRRALSAVPAVLLVLTPGLPVWAQNDTEPIVLEGKCLVVCDSPATDSKGSSSPLGI
SVRAANSKVAFSAVRSTNHEPSEMSNKTRIYFDQILVNVGNFFTLESVFVAPRKGIYSFSF
HVIKVYQSQTIQVNMLNLNGKPVISAFAGDKDVTREAATNGVLLYLDKEDKVYLKLEKGNLVG
GWQYSTFSGFLVFPL

Signal peptide:

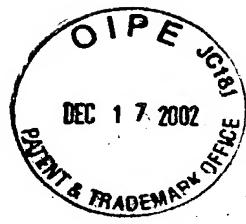
amino acids 1-27



128/249

FIGURE 127

CGGTGGCCATGACTGC GGCGT GTTCTTCGGCTGC GCCTTCATTGCCTC GGGC TGC GCTC
GCC CTTATGTCTCACCATGCCATCGAGCCGTTGCGTATCATCTTCCTCATGCCGGAGC
TTTCTTCTGGTTGGTGTCTACTGATT CGTCCCTGTTGGTCATGGCAAGAGTCATTA
TTGACAACAAAGATGGACCAACACAGAAATATCTGCTGATCTTGAGCGTTGTCTGTC
TATATCCAAGAAATGTTCCGATTGCATATTATAAACTCTTAAAAAGCCAGTGAAGGTTT
GAAGAGTATAAACCCAGGTGAGACAGCACCCCTATGCGACTGCTGGCCTATGTTCTGGCT
TGGGCTTGGAAATCATGAGTGGAGTATTTCTTGTGAATACCCTATCTGACTCCTTGGGG
CCAGGCACAGTGGGCATT CATGGAGATTCTCCTCAATTCTCCTTATT CAGCTTCATGAC
GCTGGTCATTATCTGCTGCATGTATTCTGGGCATTGTATTTTGATGGCTGTGAGAAGA
AAAAGTGGGCATCCTCCTTATCGTTCTCC TGACCCACCTGCTGGTGT CAGCCCAGACCTTC
ATAAGTTCTTATTATGGAATAAACCTGGCGTCAGCATTATAATCCTGGTGCTCATGGCAC
CTGGGCATTCTTAGCTGCCGGAGGCAGCTGCCGAAGCCTGAAACTCTGCCTGCTTGCCAAG
ACAAGAACCTTCTTTACAACCAGCGCTCCAGATAACCTCAGGGAACCAGCACTCCCAA
ACCGCAGACTACATCTTAGAGGAAGCACA ACTGTGCCTTTCTGAAAATCCCTTTCTG
GTGGAATTGAGAAAGAAATAAAACTATGCAGATA



129/249

FIGURE 128

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66658
><subunit 1 of 1, 257 aa, 1 stop
><MW: 28472, pI: 9.33, NX(S/T): 0
MTAAVFFGCAFIAFGPALALYVFTIAIEPLRIIFLIAGAFFWLVSLLISSLVWFMARVIIDN
KDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVSGLGF
GIMSGVFSFVNTLSDSLGP GTVGIHGDSPQFFLYSAFMTLVII LLHVFWGIVFFDGCEKKW
GILLIVLLTHLLVSAQTFI SYYGINLASAFIILVLMGTWAFLAAGGSCRSLKLCLLCQDKN
FLLYNQRSR

Important features of the protein:

Signal peptide:

amino acids 1-19

Transmembrane domains:

amino acids 32-51, 119-138, 152-169, 216-235

Glycosaminoglycan attachment site.

amino acids 120-123

Sodium:neurotransmitter symporter family protein

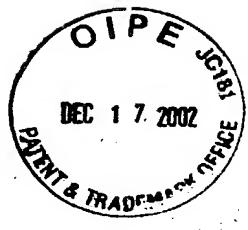
amino acids 31-65



130/249

FIGURE 129

CGGCAACCAGCCGCCACCACCGCTGCCACTGCCGCCCTGCCGGGGCC **ATGTTCGCTCTGGGCTTGCCCTTCT**
TGGTCTTGGCTCGGTGAGAGCATCTGGGGTTCTGGGGCCAAGAACGTCCTGCAGAAAGACGCC
AGTTGAGCGCACCTACGTGGACGGTCAACAGCAGCTGGTCAACATCTACACCTCAACCATACTGTGACCC
GCAACAGGACAGAGGGCGTGCCTGCTGTGAACGTCCTGAACAAGCAGAAGGGGGCGCCGTTGCTGTTGTGG
TCGCCCAGAAGGAGGCTGTGGTCTCTTCAAGGTGCCCTAATCTGCAGGGATGTTTCAGCGCAAGTACCTCT
ACCAAAAGTGGAACGAAACCTGTGTCAGCCCCCAAGAATGAGTCGGAGATTCAAGTCTTACGTGGATG
TGCCACCCCTGTCACAGTCACACACATACCAGCTCGGGTCAGCGCATGGACGATTTGTGCTCAGGACTG
GGGAGCAGTCAGCTTAATACACAGCAGCACAGCCCCAGTACTTCAGTATGAGTCCCTGAAGGCGTGGACT
CGGTAATTGTCAGGTCACAGCTCAACACATACCAGCAGCACAGCCCCAGTACTTCAGTATGAGTCCCTGAAGGCGTGGACT
TCTATGACCTGGACAACAACGTAGCCTTCATCGGATGTACAGACGATGACCAAGAAGGCGCCATACCGTAC
AGCGCAAAGACTTCCCAGCAACAGCTTTATGTGGTGGTGGTGAAGACCGAAGACCAAGCCTGCGGGGCT
CCCTGCCITTCTACCCCTCGCAGAAGATGAACCGGTGATCAAGGGCACCGCAGAAAACCTGTCAGTGTGCTGG
TGTCTCAAGCAGTCACGTCTGAGGCATACGTCACTGGGATGCTCTTGGCTGGTATATTCTCCTTCT
TGCTGACCGTCCTCTGGCCTGCTGGAGAACTGGAGGAGAAGAAGAACCCCTGCTGGTGGCATTGACCGAG
CCTGCCAGAAAGCGGTACCCCTGAGTCCTGGTGAATTCTTCTGGCAGTTCCCTTATGAGGGTTACAACT
ATGGCTCCTTGAGAAATGTTCTGGATCTACCGATGGTCTGGTGAACAGCGCTGGCAGTGGGACCTCTTAC
GTACCGAGGCCGCTCTTGAAACCTGTAGGTACTCGGCCCCAGTGGACTCCATGAGCTCTGTGGAGGAGGATG
ACTACGACACATTGACCGACATCGATTCCGACAAGAAATGTCATTGCAACAGAACATCTCTATGTGGCTGACC
TGGCACGGAAGGACAAGCGTGTCTGGGAAAAAGTACAGATCTACTCTGGAAACATTGCCACATTGCTGTCT
TCTATGCCCTCCTGTGGTGGCAGTGGTGTACCTACAGACGGTGGTGAATGTCACAGGAAATCAGGACATCT
GCTACTACAATTCTCTGCGCCCCACCCACTGGCAATCTCAGCGCTTAACAAACATCCTCAGCAACCTGGG
ACATCCTGCTGGGCTGCTTCTGCTCATCATCCTGCAACGGAGATCAACCACAAACCGGGCCCTGCTGCGCA
ATGACCTCTGTGCCCTGGAAATGTGGATCCCCAAACACTTGGGCTTTCTACGCCATGGCACAGCCCTGATGA
TGGAGGGCTGCTCAGTGTCTATCATGTGTGCCCAACTATACCAATTCCAGTTGACACATCGTTCATGT
ACATGATGCCGGACTCTGCATGCTGAAGCTTACACAGAACGCGCACCGACATCAACGCCAGCGCTACAGT
CCTACGCCCTGCCATTGTCTTCTGCTGGGCTGGCTTTGGCAAGGGAACACGGCGTTCT
GGATCGTCTCTCCATTCACATCATGCCACCCCTGCTCTCAGCACGAGCTCTATTACATGGCCGGTGG
AACTGGACTCGGGATCTCCGCCATCTCCACGTGCTCTACACAGACTGCATCCGGCAGTGCAGCGGGCC
TCTACGTGGACCGCATGGTGTCTGGTCACTGGCAACGTCAACTGGCGCTGGCTATGGGCTTATCA
TGGGCCCAATGATTGCTTCTACTGTGGCATGGCAACTCTGCTGGCTTCTACCTCCCTTCTACA
TCATCATGAAGCTCCGGAGTGGGAGAGGATCAAGCTCATCCCCCTGCTCTGCATCGTGGCT
GGGGCTTCGGCTCTCTCTTCCAGGGACTCAGCACCTGGCAGAGTCTGGCACTTCTCTCCATGCCATGTC
ACCGGGACTGCATCTCTCGACTCTTGCAGGACACGACATCTGGCACTTCTCTCCATGCCATGTC
GGCCTTCTGGTGTGACTGGATGACGACCTGGATACTGTGCAAGCGGGACAAGATCTATGTCTT**TAGC**
AGGAGCTGGCCCTCGCTCACCTCAAGGGCCCTGAGCTCTTGTGTCATAGACGGTCACTCTGTC
GTGGGGATGAGTCCCAGCAGCGTGCCAGCAGTGGATGGCAGCAGGACAGCCAGGTCTAGCTTAGGCTTGGCCT
GGGACGCCATGGGGTGGCATGGAACCTTGCAGCTGCCCTCTGCCAGGGCAGGCTGCTCCCTGGAAACCCCC
AGATGTTGGCCAAATTGCTGTTCTCAGTGTGGGCTTCCATGGGCCCTGTCCTTGGCTCTCCATT
GTCCCTTGCAAGAGGAAGGGACACCCCTCCCAATTCTCATGCCCTGCATTGGCCCTCTCCCT
ACAATGCCCAAGCCTGGACCTAAGGCCCTTTCTCCCATACTCCCACCTCAGGGCCTAGCTGGGGCCT
ATCTCTGTCTGTATCAGGGCCCAAGTCTCTTGGGCTGTCCTGGCTGCCATCACTGCCAGTCTAGCC
AGGATGGATGGGGTATGAGATTGGGGTGGCATGGCAAGCTGGTGCAGACTTGGCT
CTGGGGCAGTGCCTATTCTCTCCCTGACCTGTGCTCAGGGCTGGCTTCTAGCTTGGCT
TGAGAACGCCCTCTGATTCAAGAGGCTGAATTCAAGGGTCACTGGGCTGGCT
AGCACCAGGACTGGAGGGAGAACGCCCTCACCCCTCCCTCTTCAGGGCCTAGTCTGGCT
AGCTGGTGGCTTCTCAGTGCCTTGCACACTGCCAAGAATGTCAGGGCAAAGGAGGGATGATACAGAGTTCAG
CCCCTCTGCCCTCACAGCTGGGACCCAGTGCCTACCTTAGAAAGGGCTTCAGGAAGGGATGTGCTGTT
CCCTCTACGTGCCCTAGCCTAGCCTGCCTAGGACCCAGGGCTGGCTTAAGTTCCGTCAGTCTCAGGCA
AGTTCTGTGTTAGTCATGCACACACATACCTATGAAACCTGGAGTTACAAAGAATTGCCCAAGCTGGCAG
CCTGGCCACCCCTGGCTCTGGATCCCCCTCGTCCCACCTGGTCCACCCAGATGCTGAGGATGGGGAGCTCAGG
GGGGGCCCTGCTTTGGGATGGAATGTGTTTCTCCAAACTGTTTATAGCTGCTTGAAGGGCTGG
AGATGAGGGGGCTGGATCTTCTCAGAGCGTCCATGCTATGGTTGCATTCCGTTATGAATGAATT
TGCATTCAATAAACACCAGACTCAAAAAAAAAAAAAA



131/249

FIGURE 130

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66659
><subunit 1 of 1, 832 aa, 1 stop
><MW: 94454, pI: 6.94, NX(S/T): 12
MFALGLPFLVLLVASVESHLGVLPKNVSQKDAEFERTYVDEVNSELVNIYTFNHTVTRNRT
EGVRVSVNVLNKQKGAPLLFVVRQKEAVVSFQVPLILRGMFQRKYLYQKVERTLCQPPTKNE
SEIQFFYVDVSTLSPVNNTYQLRVSRMDFVLRTGEQFSFNTTAAQPQYFKYEFP EGVD SVI
VKVTSNKAFPCSVISI QDVLCPVYDLDNNVAFIGMYQTMTKKA ITVQRKDFPSNSFYVVVV
VKTEDQACGGSLPFYPFAEDEPV DQGH RQKTL S VL VS QAVT SEAY VSGMLFCLGI FLSFYLL
TVLLACWENWRQKKKTL LVAIDRACPESGHPRV LADSFPGSSPYEG NYGSFENVSGSTDGL
VDSAGTGDL SYGYQGRSFEPVGTRPRVDSMSSVEEDDYDTLTDIDSDKNVIRT KQYLYVADL
ARKDKRVLRK KYQIYFWNIATIAVFYALPVVQLVITYQTVVNVTGNQDICYYNFLCAHPLGN
LSAFNNILSNLGYILLGLLIIILQREINHNRALLRNDLCALECGIPKHFGLFYAMGTALM
MEGLLSACYHVC PNYTNFQFDTSF MYMIAGLCMLKLYQKRHPDINASAYSAYACLAIVIFFS
VLGVVFGKGNTAFWIVFSIIHI IATLLLSTQLYMGRWKLD SGIFRRILHVLYTDCIRQCSG
PLYVDRM VLLVMGNVINWSLAAYGLIMRPNDFASYLLAIGICNLLYFAFYIIMKLRSGERI
KLIPLL CIVCTS VVWGFALFFFQGLSTWQKTPAESREHNRDCILLDFDDHD IWHFLSSIA
MF GSFLVLLT LDDLD T VQR DKI YVF
```

Important features of the protein:

Signal peptide:

amino acids 1-18

Transmembrane domains:

amino acids 292-317, 451-470, 501-520, 607-627, 751-770

Leucine zipper pattern.

amino acids 497-518

N-glycosylation sites.

amino acids 27-30, 54-57, 60-63, 123-126, 141-144, 165-168, 364-367, 476-479, 496-499, 572-575, 603-606, 699-702



2025 RELEASE UNDER E.O. 14176

132/249

FIGURE 131

GCTCAAGTGCCCTGCCTGCCCTACCCAGCCCAGCCTGGCCAGAGCCCCCTGGAGAAGGAGC
TCTCTTCTGCTGGCAGCTGGACCAAGGGAGCCAGTCTGGCGCTGGAGGGCCTGTCCTG
ACCATGGTCCCTGCCTGGCTGTGGCTGTTGTGTCTCCGTCCCCCAGGCTCTCCCCAAGGC
CCAGCCTGCAGAGCTGTCTGGAAAGTCCAGAAAACTATGGTGGAAATTCCCTTATACC
TGACCAAGTTGCCGCTGCCCGTGAAGGGGGCTGAAGGCCAGATCGTGTGTCAGGGACTCA
GGCAAGGCAACTGAGGGCCATTGCTATGGATCCAGATTCTGGCTTCTGCTGGTGAACCAG
GCCCTGGACCGAGAGGAGCAGGCAGAGTACAGCTACAGGTACCCCTGGAGATGCAGGATG
GACATGTCTGTGGGTCCACAGCCTGTGCTGTGCACTGAAGGATGAGAATGACCAGGTG
CCCCATTCTCTCAAGCCATCTACAGAGCTCGGCTGAGCCGGGTACCAGGCCATGGCATCCC
CTTCCTCTCCTGAGGGCTTCAGACCAGGATGAGCCAGGCACAGCCAACCGATCTTCGAT
TCCACATCCTGAGCCAGGCTCCAGCCCCAGCCTCCCCAGACATGTTCCAGCTGGAGCCTCGG
CTGGGGCTCTGGCCCTCAGCCCCAAGGGGAGCACCAGCCTGACCACGCCCTGGAGAGGAC
CTACCAGCTGTTGGTACAGGTCAAGGACATGGGTGACCCAGGCCCTAGGCCACCAGGCCACTG
CCACCGTGGAAACTCTCCATCATAGAGAGCACCTGGGTGCTCCAGACCTATCACCTGGCA
GAGAATCTCAAAGCTCTATACCCGACCACTGGCCAGGTACACTGGAGTGGGGTGTATGT
GCACTATCACCTGGAGAGGCATCCCCGGGACCCATTGAAGTGAATGCAGAGGGAAACCTCT
ACGTGACCAAGAGAGCTGGACAGAGAACGCCAGGCTGAGTACCTGCTCAGGTGCGGGCTCAG
AATTCCATGGCGAGGACTATGCGCCCTCTGGAGCTGCACGTGCTGGTGTGGATGGATGAGAA
TGACAACGTGCCTATCTGCCCTCCCCGTGACCCACAGTCAGCATCCCTGAGCTCAGTCCAC
CAGGTACTGAAGTGAAGTAGACTGTCACTGAGAGGATGCAGATGCCCGGCTCCCCAATTCC
CACGTTGTGTATCAGCTCTGAGCCCTGAGCCTGAGGATGGGTAGAGGGGAGAGCCTCCA
GGTGGACCCCACCTCAGGCAGTGTGACGCTGGGGTGCTCCACTCCGAGCAGGCCAGAAC
TCCTGCTCTGGTGCCTGGCCATGGACCTGGCAGGCCAGGGTGGCTCAGCAGCACGTGT
GAAGTCGAAGTCGAGTCACAGATATCAATGATCACGCCCTGAGTTCATCACTCCCAGAT
TGGCCTATAAGCTCCCTGAGGATGTGGAGCCGGACTCTGGTGGCCATGCTAACAGCCA
TTGATGCTGACCTCGAGCCCGCCTCCGCCTCATGGATTGGAGCCAGACTCTGGGATGTTAGACTCAGACTCTGCAA
GAAGGGACTTTGGCCTGGATTGGAGCCAGACTCTGGGATGTTAGACTCAGACTCTGCAA
GAACCTCAGTTATGAGGCAGCTCCAAGTCATGAGGTGGTGGTGGTGCAGAGTGTGGCA
AGCTGGTGGGCCAGGCCAGGCCCTGGAGCCACGCCAGGTGACTGTGCTAGTGGAGAGA
GTGATGCCACCCCCAAGTTGGACCCAGGAGAGCTACGAGGCCAGTGTCCCCATCAGGCC
AGCCGGCTCTTCCTGCTGACCATCCAGCCCTCCGACCCATCAGCCGAACCCCTCAGGTTCT
CCCTAGTCATGACTCAGAGGGCTGGCTCTGCATTGAGAAATTCTCCGGGAGGTGCACACC
GCCAGTCCCTGCAGGGGCCAGGCCCTGGAGCCACCTACACGGTGCCTGTGGAGGCCAGGA
TACAGCCCTGACTCTTGCCTCTGCCCCATGCCCTCCAATACCTCTGCACACCCGCCAAGACCAG
GCTTGATCGTGAGTGGACCCAGCAAGGACCCGATCTGGCCAGTGGCACGGTCCCTACAGC
TTCACCCCTGGTCCAACCCACGGTGCACGGGATTGGCCCTCCAGACTCTCAATGGTTC
CCATGCCCTACCTCACCTTGGCCCTGCATTGGTGAGCCACGTGAACACATAATCCCCGTGG
TGGTCAGCCACAATGCCAGATGTGGCAGCTCCTGGTTGAGTGTGATCGTGTGCTGCAAC
GTGGAGGGCAGTGCATGCGCAAGGTGGCCGATGAAGGGCATGCCACGAAGCTGTCGGC
AGTGGGCATCCTGTAGGCACCCCTGGTAGCAATAGGAATCTCCTCATCCTCATTTCACCC
ACTGGACCATGTCAAGGAAGAAGGACCCGGATCAACCAGCAGACAGCGTGCCCTGAAGGCG
ACTGTC**TGA**ATGGCCCAGGCAGCTAGCTGGAGCTTGGCCTCTGGCTCCATCTGAGTCCC
CTGGGAGAGAGGCCAGCACCCAGATCCAGCAGGGACAGGACAGAGTAGAAGCCCCTCCAT
CTGCCCTGGGGTGGAGGCACCATCACCATCACAGGCATGTCAGAGGCCCTGGACACCAAC
TTTATGGACTGCCCATGGAGTGCCTCAAATGTCAGGGTGTGCCCCATAATAAGCCCCA
GAGAACTGGCTGGCCCTATGGGAAAAAAAAAAAAAAAG



133/249

FIGURE 132

MVPAWLWLLCVSVPQALPKAQPAELSVEVPENYGGNFPPLYLTKLPLPREGAEGQIVLSGDSG
KATEGPFAMDPDSGFLLVTRALDREEQAELYQLQVTLEMQDGHVLWGPQPVLVHVKDENDQVP
HFSQAIYRARLSRGTRPGIPFLFLEASDRDEPGTANSDLRFHILSQAPAQPSPD MFQLEPRL
GALALSPKGSTSLDHALER TYQLLVQVKDMGDQASGHQATATVEVSIIESTWVSLEPIHLAE
NLKVLYPHHMAQVHWSGGDVHYHLESHPPGPFEVNAEGNLYVTRELDREAQAEYLLQVRAQN
SHGEDYAAPPLELHVLMMDENDNVPICPPRDPTVSIPELSPPGTEVTRLSAEDADAPGSPNSH
VVYQLLSPEPEDGV EGRAFQVDPTSGSVTLGVPLRAGQNILLVLAMDLAGAEGGFSSSTCE
VEVAVTDINDHAPEFITSQIGPISLPEDVEPGTLVAMLTAIDADLEPAFR LMDFAIERGDTE
GTFGLDWEPDSGHVRLRLCKNLSYEAAAPSHEVVVVVQSVAKLVGPGPGPGATATVTVLVERV
MPPP KLDQESYEASVPISAPAGSFLLTIQPSDPISRTLRFSLVN DSEGWL CIEKFSGEVHTA
QSLQGAQPGDTYTVLVEAQDTALT LAPVPSQYLCTPRQDHGLIVSGPSKDPDIASGHGPYSF
TLGPNPTVQRDWRLQTLNGSHAYLT LALHWVEPREHIIPVVVSHNAQM WQLLVRVIVCRCNV
EGQCMRKVGRMKGMPTKLSAVGILVGT LVAIGIFLILIFT HWTMSRKKDPDQPADSVPLKATV

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 762-784

**FIGURE 133**

CCGGGGACATGAGGTGGATACTGTTCATGGGCCATTGGGTCCAGCATCTGTGGCAA
AAAAAATTTTGGGGACCAAGTTGAGGATTAATGTCAGAAATGGAGACGAGATCAGCAA
ATTGAGTCAACTAGTGAATTCAAACAACCTGAAGCTCAATTCTGAAATCTCCCTCCT
TCAATCGGCCTGGATGTCCTGGTCCCCTGTCACTGTCAGTCTGCAGGCATTAAATCCTCCTG
AGATCCCAGGGCTTAGAGTACGCAGTGACAATTGAGGACCTGCAGGCCCTTTAGACAATGA
AGATGATGAAATGCAACACAATGAAGGGCAAGAACGGAGCAGTAATAACTCAACTACGGG
CTTACCATCCCTGGAAGCTATTACACGAGATGGACAACATTGCCAGACCTTCCTGAC
CTGGCGAGGAGGGTGAAGATTGGACATTGTTGAAAACCGGCCGATGTATGACTGAAGTT
CAGCACTGGAAAGGCCTGAGGCAGGCCGTTGGCTGAATGCAGGCATCCATTCCGAG
AGTGGATCTCCAGGCCACTGCAATCTGGACGGCAAGGAAGATTGTATCTGATTACAGAGG
GATCCAGCTATCACCTCCATCTGGAGAAAATGGATATTCTTGTGCTGTGGCCAATCC
TGATGGATATGTGTATACTCAAACCTAAAACCGATTATGGAGGAAGACGCCGCTCCGAAATC
CTGGAAGCTCCTGCATTGGTCTGACCCAAATAGAAACTGGAACGCTAGTTGCAGGAAAG
GGAGCCAGCGACAACCCTGCTCCGAAGTGTACCATGGACCCCACGCCAATTGGAAGTGG
GGTGAATCAGTGGTAGATTTCATCCAAAAACATGGGAATTCAAGGGCTTCATCGACCTGC
ACAGCTACTCGCAGCTGCTGATGTATCCATGGTACTCAGTCAAAAGGCCAGATGCC
GAGGAACCTGACAAGGTGGCAGGGCTTGCGCCAAAGCTCTGGCTTGTGTGGGCACTGA
GTACCAAGTGGTCCCACCTGCACCACTGTCATCCAGCTAGCGGAGCAGCATCGACTGG
CGTATGACAACGGCATCAAATTGCAATTGAGTTGAGAGATACCGGGACCTATGGC
TTCCTCCTGCCAGCTAACCAAGATCATCCCCACTGCAGAGGAGACGTGGCTGGGCTGAAGAC
CATCATGGAGCATGTGCGGGACAACCTCTACTAGGGCATGGCTCTGCTCTGTACATTAT
TTGTACCCACACGTGCACGCACTGAGGCCATTGTTAAAGGAGCTTTCTACCTGTGAG
TCAGAGCCCTCTGGTTGTGGAGCACACAGGCCTGCCCTCTCCAGCCAGCTCCCTGGAGT
CGTGTGTCCCTGGCGGTGTCCTGCAAGAACTGGTCTGCCAGCCTGCTCAATTGGTCTG
CTGTTTGATGAGCCTTGTCTGTTCTCCCTGCCATGTCCTCTACCTCATTAGAACCAAGAACATC
TGAGATGATTCTCTACCCCTACACATCTAGCCAAGCCAGTGACCTGCTCTGGTGGCACT
GTGGGAGACACCACCTGTCTTAGGTGGCTCAAAGATGATGTAGAATTCTCTTAATTTC
TCGCAGTCTCCTGGAAAATTTCTTGAGCAGCAAATCTGTAGGGATATCAGTGAAG
GTCTCTCCCTCCCTCTGTTTTTTTTGAGACAGAGTTTGCTCTTGCT
CAGGCTGGAGTGTGATGGCTCGATCTGGCTCACCACACCTGCTCCCTGGGTTCAAGCA
ATTCTCCTGCCCTAGCCTTGTAGTAGCTGGTTATAGGCCATGCCACCATGCCCTGGCTA
ATTGTGTTTAGTAGAGACAGGGTTCTCCATGTTGGTCAGGCTGGCTCAAACCTCCCA
ACCTCAGGTGATGCCCTCCCTGCCCTGGCTCCAGAGTGCTGGGATTACAGGTGTGAGCCACTG
TGCCGGGCCGTCCCTCTGGCTGAATACAAAGTAGAAGATCACTTCTTCAC
TGTGCTGAGAATTCTAGATACTACAGTCTTACTCCTCTTGTATTCACTGTG
ACCAGGATGGCGGGAGGGATCTGTGTCAGTGTAGGTACTGTGCCAGGAAGGCTGGGAA
GTGACCATCTAAATTGCAAGGATGGTGAATATCCCCATCTGCTCTAAATGGGCTTACCTCCT
CTTGCCCTTGTAACTCACTCAAAGATCTAGGCCTCATCTACAGGTCTAAATCACTCAT
CTGGCCTGGATAATCTCACTGCCCTGGCACATTCCATTGTGCTGTGGTGTACCTGTGTT
TCCTTGCTCTGGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG
TCTGTCTATTGTATCCTGGACCAAGTCTCTAAAGTAGAGCAAGAATTCAACCAAGCT
GCCTCTGGTTCACTCACCTCAGCACGTACCATCTGCCTTTGTTGTTGTTGTTGTT
TTGTTTTTGCTTTACAAACATGTCTGAAATCTAACCTCCTGCCAGGATTGACA
GCATCTGGTGTGCTTATAAGCCAATAATTCAATGTGAAAAAAAAAAAAAA



135/249

FIGURE 134

MRWILFIGALIGSSICGQEKFQGDQVLRINVNGDEISKLSQLVNSNNLKLNFWKSPSSFNR
PVDVLVPSVSLQAFKSFLRSQGLEYAVTIEDLQALLDNEDEMHQNEGQERSNNFNYGAYH
SLEAIYHEMDNIAADFPDLARRVKIGHSFENRPMYVLKFSTGKVRRPAVWLNAAGIHSREWI
SQATAIWARKIVSDYQRDPAITSILEKMDIFLLPVANPDGYVYTQTQNRLWRKTRSRNPGS
SCIGADPNRNWNASFAGKGASDNPCSEVYHGPHANSEVEVKSVDIQQKHGNFKGFIDLHSY
SQLLMYPYGYSVKKAPDAEELDKVARLAAKALASVSGTEYQVGPTCTTVYPASGSSIDWAYD
NGIKFAFTFELRTGTYGFLLPANQIIPTAEETWLGLKTIMEHVRDNLY

Signal peptide:

amino acids 1-16



FIGURE 135



137/249

FIGURE 136

MASYLYGVLFAVGLCAPIYCVSPANAPSAYPRPSSTKSTPASQVYSLNTDFAFRLYRRLVLE
TPSQNIFFSPSVSTSLAMLSLGAHSVTKTQILQGLGFNLHTPESAIHQGFQHLVHSLTVP
SKDLTLKMGSALFKKELQLQANFLGNVKRLYEAEVFSTDFSNPSIAQARINSHVKKKTQGK
VVDIIQGLDLLTAMVLVNHIFFKAKWEKPFHLEYTRKNFPFLVGEQVTVQVPMMHQKEQFAF
GVDTELNCFLQMDYKGDAVAFFVLPSKGKMRQLEQALSARTLIKWSHSLQKRWIEVFIPRF
SISASYNLETILPKMGIQNAFDKNADFGIAKRDSSLQVSKATHKAVLDVSEEGTEATAATTT
KFIVRSKDGPSYFTVSFNRTFLMMITNKATDGILFLGKVENPTKS

Signal peptide:

amino acids 1-20



1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100

138/249

FIGURE 137

GGCTGACCGTGCTACATTGCCCTGGAGGAAGCCTAACGGAAACCCAGGCATCCAGCTGCCAACGC
CTGAGTCCAAGATTCTTCCCAGGAACACAAACGTAGGAGACCCACGCTCCTGGAAGCACCAG
CCTTTATCTCTTACCTTCAGTCCCCTTCTCAAGAACCTCTGTTCTTGCCCTCTAAAG
TCTTGGTACATCTAGGACCCAGGCATCTGCTTCCAGCCACAAAGAGACAGA**TGA**AAGATGC
AGAAAGGAAATGTTCTCCTTATGTTGGTCTACTATTGCAATTAGAAGCTGCAACAAATTCC
AATGAGACTAGCACCTCTGCCAACACTGGATCCAGTGTGATCTCCAGTGGAGCCAGCACAGC
CACCAACTCTGGGTCCAGTGTGACCTCCAGTGGGTCAAGCACAGCCACCATCTCAGGGTCCA
GCGTGACCTCCAATGGGTCAAGCATAGTCACCAACTCTGAGTTCCATACAACCTCCAGTGGG
ATCAGCACAGCCACCAACTCTGAGTTCAAGCACAGCGTCCAGTGGGATCAGCATAGCCACCAA
CTCTGAGTCCAGCACAAACCTCCAGTGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACAC
CCTCCAGTGGGCCAGCACAGTCACCAACTCTGGTCCAGTGTGACCTCCAGTGGAGCCAGC
ACTGCCACCAACTCTGAGTCCAGCACAGTGTCCAGTAGGGCCAGCAGCAGTGCACCAACTCTGA
GTCTAGCACACTCTCAGTGGGCCAGCACAGCCACCAACTCTGACTCCAGCACACAAACCTCA
GTGGGCTAGCACAGCCACCAACTCTGAGTCCAGCACAGCCACCAACTCTGAGTCCAGCACAGCC
ACCAACTCTGAGTCCAGCACAGTGTCCAGTAGGGCCAGCAGCAGCAGCAGCAGCAGCAGC
CACAAACCTCCAGTGGGCCAGCACAGCCACCAACTCTGAGTCCAGAACGACCTCCAATGGG
CTGGCACAGCCACCAACTCTGAGTCCAGCACGACCTCCAGTGGGCCAGCACAGCCACCAAC
TCTGACTCCAGCACAGTGTCCAGTGGGCCAGCAGCAGTGCACCAACTCTGAGTCCAGCACGAC
CTCCAGTGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACGACCTCCAGTGGGCTAGCA
CAGCCACCAACTCTGACTCCAGCACAGCCACCAACTCTGAGTCCAGCACACACCTCCAG
TCCAGCACAGTGTCCAGTGGGATCAGCACAGTCACCAATTCTGAGTCCAGCACACCCCTCCAG
TGGGCCAACACAGCCACCAACTCTGAGTCCAGTACGACCTCCAGTGGGCCAACACAGCCA
CCAACTCTGAGTCCAGCACAGTGTCCAGTGGGCCAGCAGCAGCAGCAGCAGCAGCAGC
ACAACCTCCAGTGGGTCAAGCACAGCCACCAACTCTGAGTCCAGCACACACCTCCAGTGGG
TAGCACAGCCACCAACTCTGACTCCAGCACACACCTCCAGTGGGCCAGCACAGCCACCAACT
CTGAGTCTAGCACAGTGTCCAGTGGGATCAGCACAGTCACCAATTCTGAGTCCAGCACAC
TCCAGTGGGCCAACACAGCCACCAACTCTGGTCCAGTGTGACCTCTGCAGGCTCTGGAAC
AGCAGCTCTGACTGGAATGCACACAACCTCCATAGTCATCTACTGCAGTGAGTGAGGCAA
AGCCTGGGGTCCCTGGCGTGGAAATCTCCTCATCACCCCTGGTCTCGGTTGGCG
GCCGTGGGCTTTGCTGGCTCTTCTGTGTGAGAAACAGCCTGCCCCCTGAGAAACAC
CTTTAACACAGCTGTCTACCACCCCTCATGGCCTCAACCATGGCCTTGGTCCAGGCCCTGGAG
GGAATCATGGAGCCCCCACAGGCCAGGTGGAGTCCTAAGTGGTTCTGGAGGGAGACAGTA
TCATCGATGCCATGGAGATGAGCGGGAGGAACAGCGGGCC**TGA**GCAGCCCCGGAAAGCAAG
TGCCGCATTCTCAGGAAGGAAGAGACCTGGCACCCAAAGACCTGGTTTCCTTCAATTCA
CCAGGAGACCCCTCCAGCTTGTGAGATCCTGAAAATCTGAGAAGGTATTCTCAC
TTCTGCTTACAGACACTGGAAAGAGAATACTATATTGCTCATTTAGCTAACGAAATAA
ATACATCTCATCTAACACACAGACAAAGAGAAGCTGTGCTGGCCCCGGGTGGTATCTAG
CTCTGAGATGAACCTCAGTTAGGAGAAAACCTCCATGCTGGACTCCATCTGGCATTCAAAA
TCTCCACAGTAAAATCCAAAGACCTAAAAAAAAAAAAAAA
AAAAAAA



139/249

FIGURE 138

MKMKGKGNVLLMFGLLLHLEAATNSNETSTSANTGSSVISSGASTATNGSSVTSSGVSTATISGSSVTSNGVSIVTNSEFHTTSSGISTATNSEFSTASSGISIATNSESSTSSGASTATNSESTPSSGASTVTNSGSSVTSSGASTATNSESSTVSSRASTATNSESSTLSSGASTATNSDSSTTSSGASTATNSESSTSSGASTATNSESSTVSSRASTATNSESSTSSGASTATNSESRTTSNGAGTATNSESSTSSGASTATNSDSSTVSSGASTATNSESSTSSGASTATNSESSTSSGASTATNSDSSTTSSGAGTATNSESSTVSSGISTVTNSESSTPSSGANTATNSESSTSSGANNTATNSESSTVSSGASTATNSESSTTSSGVSTATNSESSTSSGASTATNSDSSTSSEASTATNSESSTVSSGISTVTNSESSTTSSGANTATNGSSVTSAGSGTAALTGMHTTSHSASTAVSEAKPGGSLVPWEIFLITLVSVVAAVGLFAGLFFCVRNSLSLRNTFNTAVYHPHGLNHGLGPGGGNHGAPHPRPRWSPNWFWRPVSIAEMMSGRNSGP

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 510-532



140/249

FIGURE 139

GGGAGAGAGGATAAAAGCAGCGTGGCTTCCCTGGCTCCTCTGCATCCTCCGACCTTC
CCAGCAATATGCATCTGCACGTCTGGTCGGCTCCTGCTCCCTCCTGCTACTGGGGGCC
CTGTCTGGATGGCGGCCAGCGATGACCCCATTGAGAAGGTATTGAAGGGATCAACCGAGG
GCTGAGCAATGCAGAGAGAGAGGTGGCAAGGCCCTGGATGGCATCAACAGTGGAATCACGC
ATGCCGGAAGGGAAAGTGGAGAAGGTTTCAACGGACTTAGCAACATGGGAGCCACACCGGC
AAGGAGTTGGACAAAGGCGTCCAGGGCTCAACCACGGCATGGACAAGGTTGCCATGAGAT
CAACCATGGTATTGGACAAGCAGGAAAGGAAGCAGAGAAGCTTGCCATGGGTCAACAAACG
CTGCTGGACAGGCCGGGAAGGAAGCAGACAAAGCGGTCCAAGGGTCCACACTGGGTCCAC
CAGGCTGGGAAGGAAGCAGAGAAACTTGGCCAAGGGTCAACCATGCTGCTGACCAGGCTGG
AAAGGAAGTGGAGAAGCTTGGCCAAGGTGCCACCATGCTGCTGGCCAGGCCGGGAAGGAGC
TGCAGAATGCTATAATGGGTCAACCAAGCCAGCAAGGAGGCCAACCAGCTGCTGAATGGC
AACCATCAAAGCGGATCTCCAGCCATCAAGGAGGGCCACAACCACGCCGTTAGCCTCTGG
GGCCTCAGTCAACACGCCATTCAACCTTCCGCCCTGTGGAGGAGCGTCGCCAACATCA
TGCCCTAAACTGGCATCCGCCCTGCTGGAGAATAATGTCGCCGTTGTCACATCAGCTGAC
ATGACCTGGAGGGTTGGGGTGGGGACAGGTTCTGAAATCCCTGAAGGGGGTTGTA
GGATTGTGAATAAAACTTGATACACCA



141/249

FIGURE 140

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66675

><subunit 1 of 1, 247 aa, 1 stop

><MW: 25335, pI: 7.00, NX(S/T): 0

MHLARLVGSCSLLLLLGALSGWAASDDPIEKVIEGINRGLSNAEREVGKALDGINSITHAG
REVEKVFNGLSNMGSHTGKELDKGVQGLNHGMDKVAHEINHGIGQAGKEAEKLGHGVNNAAG
QAGKEADKAVQGFHTGVHQAGKEAEKLQGVNHAADQAGKEVEKLGQGAHHAAGQAGKELQN
AHNGVNQASKEANQLLNGNHQSGSSSHQGGATTPLASGASVNTPFINLPALWRSVANIMP

Important features of the protein:

Signal peptide:

amino acids 1-25

Homologous region to circumsporozoite (CS) repeats:

amino acids 35-225



2025 RELEASE UNDER E.O. 14176

142/249

FIGURE 141

CTCCGGGTCCCCAGGGGCTGCGCCGGCCGGCTGGCAAGGGGACGAGTCAGTGGACACTCCAGGAAGAGCGGC
CCCGCGGGGGCGATGACCGTGCCTGACCCCTGACTCAGTCCAGGTCCGGAGGCAGGGGCCCCGGCGACTCG
GGGGCGGACCGCGGGGGAGCTGCCGCCGTGAGTCCGCCAGGCCACCTGAGCCCAGCCGGACACCGTC
GCTCCTGCTCTCCGA**TG**CCTGCCACCCGATGGGCCCTGAGGAGCTGGCTGCCGCCCATGGGCCGCTGCC
CCTCGGCCACCGCTGCTGCTCTGCTGCTGCTGCCCTGAGCCCAGGCCACCTGAGCCCAGCCGGACACCGTC
CCCCGGATCAGCCTGCCCTGGGCTCTGAAGAGGCCATTCCAGATTGAAGCTGAACACATCTCAACTAC
ACAGCCCTCTGCTGAGCAGGGATGGCAGGCCCTGTAAGTGGGCTGAGAGGCCCTTTGCACTCAGTAGC
AACCTCAGCTTCCCTGCCAGGCCAGTACAGGAGCTGCTTGGGTGCAAGACGAGAAGAACACGAGTC
AGCTTCAAGGGCAAGGACCCACAGCGCAGTCAAAACATCAAGATCCTCCTGCCGCTCAGCGCAGTCAC
CTGTTCACCTGTGGCACAGCAGCCTCAGCCCCATGTGTACCTACATCAACATGGAGAACTTCACCCCTGGCAAGG
GACGAGAAGGGAAATGCTCTCTGGAAAGATGGCAAGGGCCTGTCACCCGAATTCAAGTCCACTGCC
CTGGTGGTTGATGGCAGCTCTACACTGGAAACAGTCAGCAGCTCCAAGGGAAATGACCCGGCATCTCGCGAGC
CAAAGCCTTCGCCCCACCAAGACCGAGAGCTCCCTCAACTGGCTGCAAGACCCAGCTTGTGGCCTCAGCCTAC
ATTCCCTGAGAGCCTGGGAGCTTGCAAGGCAGTGTGACAAGATCTACTTTTCTTCAGCGAGACTGGCCAGGAA
TTTGAGTTCTTGAGAACACCATTGTGTCCTGCCATTGCCGCTCTGCAAGGGCAGTGGCTCACGGCCGACGATGGCTTCCACT
CTACAGCAGCGCTGGACCTCCTCTCAAGGCCAGCTGCTGTGCTCACGGCCGACGATGGCTTCCACT
GTGCTGAGGATGCTCTCACGCTGAGCCCCCAGGACTGGCGTGCACACCCCTTCTATGGGTCTTCACT
TCCCAGTGGCACAGGGAACTACAGAAGGCTCTGCCCTGTCAGACAGATCTACTTCTTCAGCGAGACTTC
AGCAGCCTCTACAAGGGAGTGAACCGTGAGACACAGCAGTGGTACACCGTGACCCACCGGTGCCCACACCCCG
CCTGGAGCGTGCATCACCAACAGTGCCGGAAAGGAAGATCAACTCATCCCTGCAGCTCCAGACCGCGTGTG
AACTTCTCAAGGACCACTTCTGATGGACGGCAGGTCCGAAGCCGATGCTGCTGAGCAGCCCCAGGCTCG
TACCAAGCGCTGGCTGACCCGCTCCCTGCCCTGACCCACACCTACGATGTCTCTTCTGGCACTGGTAC
GGCCGGCTCCACAAGGCAGTGAGCGTGGGCCCTGGTCACATCATTGAGGAGCTGAGATCTCTCATCGGA
CAGCCCGTGCAGAATCTGCTCTGGACACCCACAGGGGCTGCTGTATGCCCTCACACTCGGGTAGTCCAG
GTGCCCATGGCAACTGCAGCCTGTACCGAGCTGTGGGACTGCCCTCGCCGGACCCACTGTGCTTGG
AGCGGCTCCAGCTGCAAGCACGTACGCCCTACAGCCTCAGCTGGCCACCAGGCCGTGGATCCAGGACATCGAG
GGAGCCAGCGCAAGGACCTTGCAGCGCTCTCGTTGTGTCCTCGTCTTGTACCAACAGGGAGAACCCA
TGTGAGCAAGTCCAGTCCAGCACAACACAGTGAACACTTGGCTGCCCTCCCTCCAAACCTGGCAGCCGA
CTCTGGCTACGCAACGGGCCCCCGTCAATGCCCTGCCCTCTGCCACGTGCTACCCACTGGGACCTGCTG
GTGGGACCCAAACAGCTGGGGAGTTCCAGTGTGACTAGAGGAGGCCACTCCAGCAGCTGGTAGCCAGCTAC
TGCCCAGAGGTGGAGGACGGGTGGCAGACCAAACAGATGAGGTGGCAGTGTACCCGTATTATCAGCACA
TCGCGTGTAGTGCACCAGCTGGTGGCAAGGCCAGCTGGGTGAGACAGGTCTACTGGAAGGAGTTCTGGTG
ATGTGCACGCTTTGTGCTGCCCTGCTCCCAGTTTATCTGCTACCGGCACCGAACAGCATGAAA
GTCTTCTGAAGCAGGGGAATGTGCCAGCGTGCACCCCAAGACCTGCCCTGTGGTGTGCCCCCTGAGACCCGC
CCACTCAACGGCCTAGGGCCCCCTAGCACCCGCTCGATCACCGAGGGTACCAAGTCCCTGTCAAGACAGCCCCCG
GGGGCCCAGTCTTCACTGAGTCAGAGAACAGGCCACTCAGCATCCAAGACAGCTCGTGGAGGTATCCCAGTG
TGCCCCGGCCCCGGTCCGCTTGGCTGGAGATCCGTACTCTGTGGTGT**TG**AAGCTGACTTCCAGAGGACGC
TGCCCTGGCTCAGGGCTGTGAATGCTGGAGAGGTCAACTGGACCTCCCTCCGCTCTGCTTCTGTGGAAC
ACGACCGTGGTGGCCCTTGGAGGCCCTGGAGCCAGCTGGCTGCTCTCCAGTCAAGTAGCGAAGCTCC
TACCAACAGACACCCAAACAGCGTGGCCCCAGAGGTGCTGCCAAATATGGGGCTGCCCTAGGTTGGAA
CAGTGTCTTATGTAAACTGAGCCCTTGTGTTAAAAAAACAAATCCAAATGTGAAACTAGAATGAGAGGGAGAG
ATAGCATGGCATGCAGCACACACAGGCTGCCACTTCCAGGCTGCCACAGGAGGCCAGCGAGCTCAGGAGAGA
TTGTCTGAGACAGACTGGAAACCTCACAACAGGACTGCCCTTCCAGGCTGCCACAGGAGGCCAGCGAGCT
CCTGTCTCACTGCAGATTCAAGGACAGCTGGCTGCGTCTGCCCTGCCAGTCAGCCAGGATGTAGTTG
TTGCTGCCCTGCTCCACCACCTCAGGGACAGAGGGCTAGGTTGGCACTGCCAGTCAGCCAGGATGTAGTTG
GGACCCAACTCCTGGACCTTCCAGGCTGTATCAGGCTGTGGCACACAGGAGGCCAGCGAGCTCAGGAGAGA
TTTCGTGACAATGTACGCCCTCCCTCAGAATTCAAGGAAGAGACTGTGCCCTGCCCTCCGTTGCGTG
GAACCCGTGTGCCCTCCACCATATCACCCCTGCCATCTTGAACCTAAACACAGGAGGAACACTGCACC
CTGGTCTCTCCCCAGTCCCCAGTTCAACCCCTCACCTCCACCTCCACTCTAAGGGATATCAACACTGCC
AGCACAGGGCCCTGAATTATGTGGTTTATACATTAAAGATGCACTTATGTCAATTAAATAAAA
GTCTGAAGAATTACTGTTAAAAAAAAAA



143/249

FIGURE 142

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA67962
><subunit 1 of 1, 837 aa, 1 stop
><MW: 92750, pI: 7.04, NX(S/T): 6
MLRTAMGLRSWLAAPWGALPPRPLL LLLLQPPPPTWALSPRISLPLGSEERPFLRF
EAEHISNYTALLLSRDGRTLYVGAREALFALSSNLSFLPGGEYQELLWGADAEEKQQCSFKG
KDPQRDCQNYIKILLPLSGSHLFTCGTAAFSPMCTYINMENFTLARDEKGNVLLLEDGKGRC
FDPNFKSTALVVDGELYTGTVSSFQGNDPAISRSQLRPTKTESSLNLQDPAFVASAYIPE
SLGSLQGDDDKIYFFFSETGQEFEFFENTIVSRIARICKGDEGGERVIQQRWTSFLKAQLLC
SRPDDGFPFNVLQDVFTLSPSPQDWRTLTYGVFTSQWHRGTTEGSACVFTMKDVQRVFSG
LYKEVNRETQQWYTWTVPVPTPRPGACITNSARERKINSSLQLPDRVILNFLKDHFMDGQVR
SRMLLQHQARYQRVAVHRVPGLHHTYDVLFLGTGDGRHLKAVSVGPRVHIIEELQIFSSGQ
PVQNLLLDTHRGLLYAASHSGVVQPMANCSLYRSCGDCLLARDPYCAWSGSSCKHVSLYQP
QLATRPWIQDIEGASAKDLCASSVVSPSFVPTGEKPCEQVQFQPNTVNTLACPLLSNIATR
LWLRNGAPVNASASCHVLPTGDLLLVTQQLGEFQCWSLEEGFQQLVASYCPEVVEDGVADQ
TDEGGSVPIIISTSRVSAPAGGKASWGADRSYWKFLVMCTLFLVAVLLPVLFLYRHRNSM
KVFLKQGECASVHPKTCPVVLPPETRPLNGLGPPSTPLDHRGYQSLSDSPPGARVFTESKR
PLSIQDSFVEVSPVCPRPRVRLGSEIRDSVV

Transmembrane domains:

amino acids 23-46 (type II), 718-738



FIGURE 143A



145/249

FIGURE 143B

TTAATTTTATATTCTTACTGTTTACTAAATATTAAGTGTCTTGACAATTTGGTGCTCATGTGTTGGG
GACAAAAGTGAATGAATCTGTCATTATACCAGAAAAGTTAAATTCAGATCAAATGTGCCTTAATAAATTGTT
TTCATTTAGATTCAAACAGTGATAGACTTGCCATTAAATACACGTCTGGAGGGCTGCGTATTTGTAATAG
CCTGATGCTCATTGGAAAAATAAACCAAGTGAACAAATATTTCTATTGTACTTTCGAACCAACCTTGTCTCATT
ATTCCTGTTAGCTGAAGAATTGTATTACATTGGAGAGTAAAAAACTTAAACACGAAAAAA



146/249

FIGURE 144

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68836
><subunit 1 of 1, 802 aa, 1 stop
><MW: 91812, pI: 9.52, NX(S/T): 3
MAARGRRAWLSVLLGLVLGFVLASRLVLPRASELKragPrrrasPEGcrsgQAAASQAGGAR
GDARGAQLWPPGSDPDGGPRDRNFLFVGVMTAQKYLQTRAVAAYRTWSKTIPGKVQFFSSEG
SDTSVPPIPVPVPLRGVDDSYPPQKKSFMMLKYMHDHYLDKYEWFMRAADDVYIKGDRLENFLR
SLNSSEPLFLGQTGLGTTEEMKLALEPGENFCMGGPGVIMSREVLRRMVPHIGKCLREMYT
THEDVEVGRCVRRFAGVQCVWSYEMRQLFYENYEQNKKGYIRDLHNSKIHQAITLHPNKNPP
YQYRLHSYMLSRKISELRHRTIQLHREIVLMSKYSNTEIHKEDELQLGIPPSFMRFQPRQREE
ILEWEFLTGKYLYSAVDGQPPRRGMDSAQREALDDIVMQVMEMINANAKTRGRIIDFKEIQY
GYRRVNPMYGAEYILDLLLLYKKHKGMTPVRRHAYLQQTFSKIQFVEHEELDAQELAKR
INQESGSLSFLNSLKKLVPFQLPGSKSEHKEPKDKKINILIPLSGRFDMFVRFMGNFEKTC
LIPNQNWKLVVLLFNNSDSNPDKAKQVELMRDYRIKYPKADMQILPVSGEFSRALALEVGSSQ
FNNESLLFFCDVDLVFTTEFLQRCRANTVLGQQIYFPIIFSQYDPKIVYSGKVPSDNHFAFT
QKTGFWRNYGFGITCIYKGDLVRVGGFDVSIQGWGLEDVDFNKVVQAGLTFRSQEVGVVH
VHHPVFCDPNLDPKQYKMCLGSKASTYGSTQQLAEMWLEKNDPSYSKSSNNNGSVRTA
```

Signal peptide:

amino acids 1-23



147/249

FIGURE 145

GGACAACC GTT GCT GGG GTCC AGGG C T GAGG CAGG AC GG TACT CCG CT GAC AC CCT TCCC
TT CGGC TT GAGG TT CCC AGC CT GG TG GCCCC AGG AC GT CC GG TC GAT GG CAG AGT GCT
AC GG AC GAC GC CT **ATGA** AGC CCT TAG C TT CT AG TT GCG CTT GCT AT GG CCT TCG TCT G
TG CGC TT AT CG AGC ATA ACT GT GAC AC CT GAT GAAG AGC AAA ACT TGA AT CATT A TATA
CAAG TTT AGAGA ACCT AGT AC GAAG TGT CC CT GGG GAG CC AGG TCG T GAG AAAA ATC
TA ACT CT CCAAA ACAT GTT ATT CT AT AGC AT CAA AGG AT CAA AA ATT AAGG AGC TAG TTA
CAC AT GG AGA GCG CT CA ACT GAGA AT GAT GTT TA ACCA AT CCT AT CAGT GAAG AA ACT ACA
ACT TT CC CT AC AGG AGG CT TC AC ACC GG AA AT AGG AA AG AAAA AC AC AC GG AA AGT ACC CC
ATT CT GG TCG AT CAA ACCA AA CA AT GTT CC ATT GTT GCA TGC AG AGG AAC CT TAT ATT G
AAA AT GAAG AGC CAG AGC CAG AGC CCG AG CC AG CT GCA AA AC AA ACT GAGG CAC CA AGA AT G
TT GCC AGT GT TACT GA AT CAT CT AC AGT CC AT AT GT TAC CT CA AC AGT CAC CT GT CAC
CA CT T TAG AT AAG AGC ACT GG CATT GAG AT CT CT AC AGA AT CAG AAG AT GT CC CT CAG CT CT
CAG GT GAA ACT GCG AT AG AAA ACC CGA AG AG TTT GG AA AG CAC CC AG AG AG TTT GG AA ATA AT
GAT GAC ATT T GAAAAA ATT TAG AT ATT CACA AGT GCA AC AGG CACT TCT TAGT GA
CAC CAG CA ACC CAG C AT AT AGAGA AG AT ATT GAAG C CT C TAA AG AT CAC CT AAA AC GA AG CC
TT GCT CT AG CAG CAG CAG CAG A AC AT AA ATT AAA AC AT GT TATA AGT CCC AGT T ATT GCA
GT AGG AGC A AC AG TA AT AAA ATT GAT GAC AT CGA AC AT GT TATA AC AT GCT GT TA ATT C
TAG AT CT AA AC T CT AT GA AT ATT TAG AT ATT AA AT GT GT TAG AT CA AGG AG AG T CAC AG C CT TATT A
AA AG TTT ATT **TAA** AC A AT A AT AAA ATT TAA AC CT ACT T GAT ATT CC AT A AC AA AG CT GA
TT AAG CAA ACT GC AT TTT CAC AGG AGA AT A AT C AT ATT CG TA ATT CAA AG TT GT TAT GA AC A
ATT TT C AT AT G C ACT AAA AC CT A ATT TAA A AT AAA ATT TT GG TT CAGG AAAA



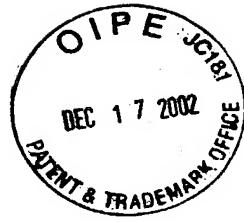
148/249

FIGURE 146

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68864
><subunit 1 of 1, 350 aa, 1 stop
><MW: 39003, pI: 5.59, NX(S/T): 1
MKPLVLLVALLLWPSSVPAYPSITVTPDEEQNLNHYIQVLENLVRSPSGEPGREKKSNSPK
HVYSIASKGSKFKELVTHGDASTENDVLTNPISEETTFPTGGFTPEIGKKKTESTPFWSI
KPNNVSIVLHAEPPYIENEPEPEPAAKQTEAPRMLPVVTESSSPYVTSYKSPVTTLDK
STGIEISTESEDVPQLSGETAIEKPEEFGKHPESWNNDILKKILDINSQVQQALLSDTSNP
AYREDIEASKDHLKRSLALAAAEEHKLKTMYKSQLLPGRTSNKIDDIETVINMLCNSRSKL
YEYLDIKCVPPEMREKAATVFNTLKNMCRSRRVTALLKVY
```

Signal peptide:

amino acids 1-19



149/249

FIGURE 147

CGGCTCGAGCGGCTCGAGTGAAGAGCCTCTCCACGGCTCCTGCGCCTGAGACAGCTGGCCTG
ACCTCCAAATCATCCATCCACCCCTGCTGTCATCTGTTTCATAGTGTGAGATCAACCCACA
GGAATATCCATGGCTTTGTGCTCATTTGGTCTCAGTTCTACGAGCTGGTGTCAAGGACA
GTGGCAAGTCACTGGACGGGCAAGTTGTCCAGGCCTGGTGGGGAGGACGCCGTGTTCT
CCTGCTCCCTTTCTGAGACCAGTGCAGAGGCTATGGAAGTGCAGGTTCTCAGGAATCAG
TTCCATGCTGTGGTCCACCTCTACAGAGATGGGAAGACTGGAATCTAACAGAGATGCCACA
GTATCGAGGGAGAAGTGAAGGACTCCATTGCAGGGGGCGTGTCTCTAACAG
TAAAAAAACATCACTCCCTCGGACATCGGCCTGTATGGGTGCTGGTCAGTTCCCAGATTAC
GATGAGGAGGCCACCTGGGAGCTGCGGGTGGCAGCAGTGGCTCACTCCTCTCATTCCAT
CGTGGGATATGTTGACGGAGGTATCCAGTTACTCTGCCTGTCCTCAGGCTGGTCCCCAGC
CCACAGCCAAGTGGAAAGGTCCACAAGGACAGGATTGTCTCAGACTCCAGAGCAAATGCA
GATGGGTACAGCCTGTATGATGTGAGATCTCATTATAGTCCAGGAAAATGCTGGAGCAT
ATTGTGTTCCATCCACCTTGCTGAGCAGAGTCATGAGGTGGAATCCAAGGTATTGATAGGAG
AGACGTTTTCCAGCCCTCACCTGGCCTGGCTTCTATTACTCGGGTTACTCTGTGGT
GCCCTGTGTGGTGTGTCATGGGATGATAATTGTTCTCAAATCCAAGGGAAAATCCA
GGCGGAACTGGACTGGAGAAGAACGACGGACAGGCAGAATTGAGAGACGCCGGAAACACG
CAGTGGAGGTGACTCTGGATCCAGAGACGGCTACCCGAAGCTCTGCCTTGATCTGAAA
ACTGTAACCCATAGAAAAGCTCCCCAGGAGGTGCCTCACTCTGAGAAGAGATTACAAGGAA
GAGTGTGGTGGCTCTCAGGGTTCCAAGCAGGGAGACATTACTGGGAGGTGGACGTGGAC
AAAATGTAGGGTGGTATGTGGAGTGTGTCGGGATGACGTAGACAGGGGAAGAACAAATGTG
ACTTTGTCTCCCAACAATGGGTATTGGGTCTCAGACTGACAACAGAACATTGTATTCAC
ATTCAATCCCCATTATCAGCCTCCCCCAGCACCCCTCCTACACGAGTAGGGTCTTCC
TGGACTATGAGGGTGGGACCATCTCCTCTCAATACAAATGACCAGTCCCTTATTATACC
CTGCTGACATGTCAGTTGAAGGCTTGTGAGACCCATATCCAGCATGCGATGTATGACGA
GGAAAAGGGACTCCCATTATCATATGTCAGTGTCTGGGATGAGACAGAGAACCCCTG
CTTAAAGGGCCCCACACCACAGACCCAGACACAGCCAAGGGAGAGTGCCTCCGACAGGTGGC
CCCAGCTCCTCTCCGGAGCCTGCGCACAGAGAGTCACGCCCTACTCTCCTTAGGGAGC
TGAGGTTCTCTGCCCTGAGCCCTGAGCAGCAGGGCAGTCACAGCTCCAGATGAGGGGGAT
TGGCCTGACCCTGTGGGAGTCAGAAGCCATGGCTGCCCTGAAGTGGGGACGGAATAGACTCA
CATTAGGTTAGTTGTGAAAACCTCCATCCAGCTAACGATCTGAACAAAGTCACAACCTCC
CAGGCTCCTCATTGCTAGTCACGGACAGTGTGATTCTGCCTCACAGGTGAAGGATTAAGAGA
CAACGAATGTGAATCATGCTTGCAGGTTGAGGGCACAGTGTGCTAATGATGTGTTTA
TATTATACATTTCCCACCATAAACTCTGTTGCTTATTCCACATTAATTACTTTCTCTA
TACCAAATCACCCATGGAATAGTTATTGAACACACTGCTTGTGAGGCTCAAAGAATAAGAG
GAGGTAGGATTTCACTGATTCTATAAGCCCAGCATTACCTGATACCAAAACCAGGCAAAG
AAAACAGAAGAAGAGGAAGGAAAACACAGGTCCATATCCCTCATTAACACAGACACAAAAAA
TTCTAAATAAAATTAAACAAATTAAACTAAACAAATATATTAAAGATGATATATAACTACT
CAGTGTGGTTGTCCCACAAATGCAGAGTTGGTTAATATTAAATATCAACCAGTGTAAATT
CAGCACATTAATAAGTAAAAAGAAAACCATAAAAAAAAAAAAAAA



150/249

FIGURE 148

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68866
><subunit 1 of 1, 466 aa, 1 stop
><MW: 52279, pI: 6.16, NX(S/T): 2
MAFVLILVLSFYELVSGQWQVTGPGKFKVQALVGEDAVFSCSLFPETSAEAMEVRFFRNQFHA
VVHLYRDGEDWESKQMPQYRGRTEVKDSIAGGRVSLRLKNITPSDIGLYGCWFSSQIYDEE
ATWELRVAALGSLPLISIVGYVDGGIQLLCLSSGWFPQPTAKWKGPQGQDLSSDSRANADGY
SLYDVEISIIVQENAGSILCSIHLAEQSHEVESKVLIGETFFQPSPWRLASILLGLLCALC
GVVMGMIIVFFKSKGKIQAELDWRRKHGQAEELRDARKHAVEVTLDPETAHPKLCVSDLKTVT
HRKAPQEVPHSEKRFTRKSVASQGFQAGRHYWEVDVGQNVGWWVGVCRDDVDRGKNNVTLS
PNNGYWVLRLTTEHLYFTFNPHFISLPPSTPPTRGVFLDYEGGTISFFNTNDQSLIYTLLT
CQFEGLLRPYIQHAMYDEEKGTPIFICPVSWG
```

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 131-150, 235-259



151/249

FIGURE 149

CCTTCACAGGACTCTCATTGCTGGTGGCAATGATGTATCGGCCAGATGTGGTGAGGGCTA
GGAAAAGAGTTGTTGGGAACCCCTGGGTTATCGGCCTCGTCATCTCATATCCCTGATTGTC
CTGGCAGTGTGCATTGGACTCACTGTTCATATGTGAGATATAATCAAAAGAACCTACAA
TTACTATAGCACATTGTCATTACAAC TGACAAACTATATGCTGAGTTGGCAGAGAGGGCTT
CTAACAAATTACAGAAATGAGCCAGAGACTTGAATCAATGGTAAAAATGCATTTATAAA
TCTCCATTAAGGGAAAGAATTGTCAAGTCTCAGGTTATCAAGTTCAAGTCAACAGAACATGG
AGTGTGGCTCATATGCTGTTGATTGTAGATTCACTCTACTGAGGATCCTGAAACTGTAG
ATAAAATTGTTCAACTGTTTACATGAAAAGCTGCAAGATGCTGTAGGACCCCCCTAAAGTA
GATCCTCACTCAGTTAAAATTAAAAAAATCAACAAAGAACAGAACAGACAGCTATCTAACCA
TTGCTGCGGAACACGAAGAAGTAAAACCTCTAGGTCAAGTCTCAGGATCGTTGGACAG
AAGTAGAAGAGGGTGAATGCCCTGGCAGGCTAGCCTGCAGTGGATGGAGTCATCGCTGT
GGAGCAACCTTAATTAAATGCCACATGGCTTGTGAGTGCTGCTCACTGTTAACACATATAA
GAACCCCTGCCAGATGGACTGCTTCCTTGGAGTAACAATAAACCTTCGAAAATGAAACGGG
GTCTCCGGAGAATAATTGTCCATGAAAATACAAACACCCATCACATGACTATGATATTCT
CTTGCAGAGCTTCTAGCCCTGTTCCCTACACAAATGCAGTACATAGAGTTGTCTCCCTGA
TGCATCCTATGAGTTCAACCAGGTGATGTGATGTTGTGACAGGATTGGAGCAGTAAAA
ATGATGGTTACAGTCAAATCATCTCGACAAGCACAGGTGACTCTCATAGACGCTACA
TGCAATGAACCTCAAGCTACAATGACGCCATAACTCCTAGAATGTTATGTGCTGGCTCCT
AGAAGGAAAAACAGATGCATGCCAGGGTGA CTTGGAGGACCACTGGTAGTTAGTCAGATGCTA
GAGATATCTGGTACCTGCTGGAATAGTGAGCTGGGAGATGAATGTGCGAAACCCAACAAG
CCTGGTGT TATACTAGAGTTACGCCCTGCGGGACTGGATTACTTCAAAAACTGGTATCTA
AGAGACAAAAGCCTCATGGAACAGATAACATT TTTTTGTTTTGGGTGTGGAGGCCATT
TTTAGAGATAAGAATTGGAGAAGACTTGCAAAACAGCTAGATTGACTGATCTAATAAAC
TGTGTTGCTGATGCATGTATTTCTTCCCAGCTCTGTTCCGCACGTAAGCATCCTGCTTCTG
CCAGATCAACTCTGCATCTGTGAGCAATAGTTATGTACATAGAGAAATAGATA
ATACAATATTACATTACAGCCTGTATTCTAGAAGTTGTCAAGTCTGAGAATTGAC
TTGTTGACATAAATTGTAATGCATATATAACATTGAAAGACTCCATTTCAGGACTCCTTCTCAGTTCTC
AGCTCCTCTCATTCAGCAAATATCCATTTCAGGTCAGAACAGGAGTGAAAGAAAATA
TAAGAAGAAAAAAATCCCCTACATT TATTGGCACAGAAAAGTATTAGGTGTTTTCTTAGT
GGAATATTAGAAATGATCATATTCAAGGTCAGAACAGACAGCAGAACATACCAATC
ACTTCATCATTAGGAAGTATGGAACTAAGTTAAGGAAGTCCAGAAAGAACAGATATA
TCCTTATTCATTCCAAACAACACTACTATGATAAATGTGAAGAAGATTCTGTTTTGTG
ACCTATAATAATTACAAACTTCATGCAATGTACTGTTCTAAGCAAATTAAAGCAAATAT
TTATTTAACATTGTTACTGAGGATGTCAACATATAACAAATAAAATATAACCCCA



152/249

FIGURE 150

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68871
><subunit 1 of 1, 423 aa, 1 stop
><MW: 47696, pI: 8.96, NX(S/T): 3
MMYRPDVVRARKRVCWEPWVIGLVIFISLIVLAVCIGLTVHYVRYNQKKTNYYSTLSFTTD
KLYAEFGREASNNFTEMSQRLESMVKNAYKSPLREEFVKSQVIKFQQKHGVLAHMLLICR
FHSTEDPETVDKIVQLVLHEKLQDAVGPPKVDPHSVKIKKINKTETDSYLNHCCGTRRSKTL
GQSLRIVGGTEVEEGEWPWQASLQWDGSHRCATLINATWLVSAAHCFTTYKNPARWTASFG
VTIKPSKMKRGLRRIIVHEKYKHPSHDYDISLAELSSPVYNAVHRVCLPDASYEFQPGDV
MFVTGFGALKNDGYSQNHLRQAQVTLIDATTNEPQAYNDAITPRMLCAGSLEGKTDACQGD
SGGPLVSSDARDIWYLAGIVSWGDECAKPNKPGVYTRVTALRDWITSKTGI

Transmembrane domain:

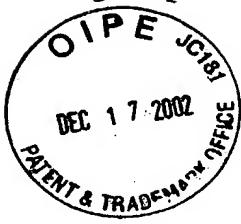
amino acids 21-40 (type II)



153/249

FIGURE 151

GTCGAAGGTTATAAAAGCTTCCAGCAAACGGCATTGAAGTTGAAGATACAACCTGACAGCA
CAGCCTGAGATCTGGGATCCCTCAGCCTAACACCCACAGACGTAGCTGGTGGATTCCCG
CTGCATCAAGGCCTACCCACTGTCTCCATGCTGGCTCTCCCTGCCTTCTGTGGCTCCTGGC
CGTGACCTTCTTGGTCCCAGAGCTCAGCCCTGGCCCCCTAAGACTTGAAGAAGAGGAGG
CAGATGAGACTGAGACGGCGTGGCCGCCTTGCCGGCTGTCCCCTGCGACTACGACCAC TG
CGACACCTGCAGGTGCCCTGCAAGGAGCTACAGAGGGCTGGCCGGCGCTGCCTGTGCC
AGGACTCTCCAGCCCCGCCAGCCGCCGACCCGCGCATGGAGAAGTGCCTACGGCG
CCGAAGAGGGCCGCGCAGTGGTCCACTGGTGTGCCCTCTCCCCGGTCTCCACTACTGG
CTGCTGCTTGGGACGGCAGCGAGGCTGCGCAGAAGGGCCCCGCTGAACGCTACGGTCCG
CAGAGCCGAACTGAAGGGCTGAAGCCAGGGGCATTTATGCGTTGCGTAGTGGCCGCTA
ACGAGGCCGGGCAAGCCCGTGCCCCAGGCTGGAGGAGAGGGCCTCGAGGGGCCGACATC
CCTGCCTCAGGGCTTGCAAGCCGCTTGCGGTGCCGCCAACCCCGCACTCTGGTCCACGC
GGCGCTGGGGTGGCACGGCCCTGGCCCTGCTAAGCTGTGCCGCCCTGGTGTGGCACTTCT
GCCTGCCTGGGGCTGCCCGCCGAGCCGCCGAGCCGAGGGCGCTCTGA
AAGGGGCCTGGGGCATCTGGCACAGACAGCCCCACCTGGGGCGCTCAGCCTGGCCCCG
GGAAAGAGGAAAACCGCTGCCTCCAGGGAGGGCTGGACGGCGAGCTGGAGCCAGCCCCAG
GCTCCAGGGCCACGGCGGAGTCATGGTCTCAGGACTGAGCGCTTGTAGGTCCGGTACTT
GGCGCTTGTTCCTGGCTGAGGTCTGGGAAGGAATAGAAAGGGCCCCAATTTTTTTA
AGCGGCCAGATAATAATAATGTAACCTTGCCTTGGTAAAAAAA



154/249

FIGURE 152

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68874
><subunit 1 of 1, 238 aa, 1 stop
><MW: 25262, pI: 6.44, NX(S/T): 1
MLGSPCLLWLLAVTFLVPRAQPLAPQDFEEEEADETETAWPPLPAVPCDYDHCRHLQVPCKE
LQRVGPAACLCPGLSSPAQPPDPPRMGEVRIAAEEGRAVVHWCAPFSPVLHYWLLLWDGSEA
AQKGPPLNATVRRAELKGLKPGGIYVVCVVAANEAGASRVPQAGGELEGADIPAFGPCSRL
AVPPNPRTLVHAAVGVGTALALLSCAALVWHFCLRDRWGCPRRAAARAAGAL
```

Important features of the protein:

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 194-220

N-glycosylation site.

amino acids 132-135



155/249

FIGURE 153

AGAGAAAGAACGCTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCGCGAAGAAGTTCC
CTGCCCGATGAGCCCCCGCCGTGCGTCCCCGACTATCCCCAGGCAGGGCTGGGGCACCGGG
CCCAGCAGCGACATCGCTGCCGTTGCCCTGGGAGTAGGATGTGGTGAAAGGATGGGC
TTCTCCCTACGGGCTCACAAATGCCAGAGAAGATTCCGTGAAGTGTCTGCCTGCCTGCT
CTACGCCCTCAATCTGCTCTTGGTTAATGTCCATCAGTGTGGCAGTTCTGCTTGG
TGAGGGACTACCTAAATAATGTTCTCACTTAACATGCAGAAACGAGGGTAGAGGAAGCAGTC
ATTTGACTTACTTCCTGTGGTCATCCGGTCATGATTGCTGTTGCTGTTCCATTATCAT
TGTGGGATGTTAGGATATTGTGGAACGGTAAAAGAAATCTGTTGCTTCTGCAATGGTACT
TTGGAAGTTGCTGTCAATTCTGTGTAGAAACTGGCTGTGGCCTGGACATATGAACAG
GAACCTATGGTCCAGTACAATGGTCAGATATGGTCACCTTGAAAGCCAGGATGACAAATTA
TGGATTACCTAGATATCGGTGGCTACTCATGCTTGAATTTCAGAGAGAGTTAAGT
GCTGTGGAGTAGTATATTCACTGACTGGTGGAAATGACAGAGATGGACTGGCCCCAGAT
TCCTGCTGTGTAGAGAAATTCCCAGGATGTCCAAACAGGCCACCAGGAAGATCTCAGTGA
CCTTATCAAGAGGGTGTGGGAAGAAAATGTATTCTTTGAGAGGAACAAACAACTGC
AGGTGCTGAGGTTCTGGGAATCTCCATTGGGTGACACAAATCCTGCCATGATTCTCACC
ATTACTCTGCTCTGGCTCTGTATTATGATAGAAGGGAGCCTGGACAGACAAATGATGTC
CTTGAAGAATGACAACCTCAGCACCTGTCACTGCTTCAAGTAGAAACTGTTGAAACCAAGCC
TGTCAAGAATCTTGAACACACATCCATGGCAAACAGCTTAAATACACACTTGAGATGGAG
GAGTTATAAAAAGAAATGTCACAGAAAGAAAACCACAAACTGTTTATTGGACTTGTGAATT
TTTGAGTACATACTATGTGTTCAGAAATATGTAGAAATAAAATGTGCCATAAAATAACA
CCTAACGATATACTATTCTATGCTTAAATGAGGATGGAAAAGTTCACTGTCATAAGTCAC
CACCTGGACAATAATTGATGCCCTAAATGCTGAAGACAGATGTCAACCCACTGTGTAGC
CTGTGTATGACTTTACTGAACACAGTTATGTTTGAGGCAGCATGGTTGATTAGCATTTC
CGCATCCATGCAAACGAGTCACATATGGTGGACTGGAGCCATAGTAAAGGTTGATTACTT
CTACCAACTAGTATATAAGTACTAATTAAATGCTAACATAGGAAGTTAGAAAATACTAATA
ACTTTATTACTCAGCGATCTATTCTCTGATGCTAAATAATTATATCAGAAAACCTTC
AAATTGGTACTACCTAAATGTGATTTGCTGGTTACTAAATATTCTTACCAACTAAAA
GAGCAAGCTAACACATTGTCTTAAGCTGATCAGGGATTTGTATATAAGTCTGTGTAAA
TCTGTATAATTCACTGATTCTGATAATGTTAAGAATAACCATTATGAAAAGGAAA
ATTGTCCTGTATAGCATATTATTTAGCCTTCTGTTAATAAAAGCTTACTATTCTGT
CCTGGGCTTATATTACACATATAACTGTTATTAAATCTAACCAACTAATTGAAAATTA
CCAGTGTGATACATAGGAATCATTATTCAAGATGTAGTCTGGTCTTAGGAAGTATTAATAA
GAAAATTGCACATAACTTAGTTGATTCAAGAAAGGACTTGTATGCTGTTTCTCCAAATG
AAGACTCTTTGACACTAAACACTTTAAAAGCTTATCTTGCCTCTCCAAACAAAGAA
GCAATAGTCTCAAGTCAATATAAATTCTACAGAAAATAGTGTCTTTCTCCAGAAAAT
GCTTGTGAGAATCATTAAACATGTGACAATTAGAGATTCTTGTGTTATTCACTGATTA
ATATACTGTGGCAAATTACACAGATTATAAATTGTTACAAGAGTATAGTATATTATTT
GAAATGGGAAAAGTGCATTACTGTATTTGTGATTTGTTATTCTCAGAATATGGAA
AGAAAATAAATGTCATAAAATATTCTAGAGAGTAA



U. S. PATENT AND TRADEMARK OFFICE

156/249

FIGURE 154

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68880
><subunit 1 of 1, 305 aa, 1 stop
><MW: 35383, pI: 5.99, NX(S/T): 0
MAREDSVKCLRCLLYALNLLFWLMSISVLAWSAWMRDYLNNVLTLTAETRVEEAVILTYFPV
VHPVMIAVCCFLIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELMVPVQ
WSDMVTLKARMNTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTEMDWPPDSCCVREF
PGCSKQAHQEDLSLDLYQEGCGKKMYSFLRGTKQLQVLRFGLGISIGVTQILAMILTITLLWAL
YYDRREPGTDQMMSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHFEMEEL
```

Signal peptide:

amino acids 1-33

Transmembrane domains:

amino acids 12-35, 57-86, 94-114, 226-248



157/249

FIGURE 155

GAGAGAGGCAGCAGCTGCTCAGCGACAAGGATGCTGGCGTGAGGGACCAAGGCCTGCC
TGCACTCGGGCCTCCCTCCAGCCAGTGCTGACCAGGGACTTCTGACCTGCTGCCAGCCAGGA
CCTGTGTGGGGAGGCCCTCTGCTGCCTTGGGTGACAATCTCAGCTCCAGGCTACAGGGAG
ACCGGGAGGATCACAGAGCCAGC**ATG**TACAGGATCCTGACAGTGATCAACCTCTGAACAGC
CTCGATGTCAAACCCCTGCGCAAACCCGTATCCCCTGAGACCTTCAGAAAGGTGGGAT
CCCCATCATCATAGCACTACTGAGCCTGGCGAGTATCATCATTGTGGTTGTCCCTCATCAAGG
TGATTCTGGATAAATACTACTTCCCTCTGCGGGCAGCCTCTCCACTTCATCCGAGGAAGCAG
CTGTGTGACGGAGAGCTGGACTGTCCCTTGGGGAGGACGAGGAGCAGTGTCAAGAGCTT
CCCCGAAGGGCCTGCAGTGGCAGTCCGCCTCTCCAAGGACCGATCCACACTGCAGGTGCTGG
ACTCGGCCACAGGAACTGGTTCTCTGCCTGTTGACAACCTCACAGAACGCTCTCGCTGAG
ACAGCCTGTAGGCAGATGGCTACAGCAGAGCTGTGGAGATTGGCCAGACCAGGATCTGGA
TGTTGTTGAAATCACAGAAAACAGCCAGGAGCTTGCATGCGGAACACTCAAGTGGCCCTGTC
TCTCAGGCTCCCTGGCTCCCTGCACTGTCTGCCTGTGGGAAGAGCCTGAAGAACCCCCGT
GTGGTGGGTGGGGAGGAGGCCTCTGTGGATTCTTGGCCTTGGCAGGTCAAGCATCCAGTACGA
CAAACAGCACGTCTGTGGAGGGAGCATCCTGGACCCCCACTGGTCCTCACGGCAGCCCAC
GCTTCAGGAAACATACCGATGTGTTCAACTGGAAGGTGCGGGCAGGCTCAGACAAACTGGC
AGCTTCCCACATCCCTGGCTGTGGCAAGATCATCATCATTGAATTCAACCCATGTACCCAA
AGACAATGACATCGCCCTCATGAAGCTGCAGTTCCACTCACTTCTCAGGCACAGTCAGGC
CCATCTGTCTGCCCTTTGATGAGGAGCTCACTCCAGCCACCCACTCTGGATCATTGGA
TGGGGCTTACGAAGCAGAATGGAGGGAAAGATGTCTGACATACTGCTGCAGGCAGTCCA
GGTCATTGACAGCACACGGTCAATGCAGACGATGCGTACCGAGGGAAAGTCACCGAGAAGA
TGATGTGTGCAGGCATCCCGAAGGGGGTGTGGACACCTGCCAGGGTACAGTGGTGGGCC
CTGATGTACCAATCTGACCAAGTGGCATGTGGTGGCATGTTAGCTGGGCTATGGCTGCC
GGGCCAGCAGCCACAGGAGTACACCAAGGTCTCAGCCTATCTCAACTGGATCTACAATG
TCTGGAAGGCTGAGCTG**TAAT**TGCTGCCCTTGCACTGCTGGAGCCGCTTCCCTG
CCCTGCCACCTGGGATCCCCAAAGTCAGACACAGAGCAAGAGCTCCCTGGTACACCC
CTCTGCCACAGCCTCAGCATTCTGGAGCAGCAAAGGCCTCAATTCTGTAAGAGACCC
TCGCAGCCCAGAGGCGCCAGAGGAAGTCAGCAGCCCTAGCTGCCACACTGGTGCTCCC
AGCATCCCAGGGAGAGACACAGCCCAGTGAACAAGGTCTCAGGGTATTGCTAAGCCAAGAA
GGAACCTTCCCACACTACTGAATGGAAGCAGGCTGTCTGAAAAGCCCAGATCACTGTGG
CTGGAGAGGAGAAGGAAGGGTCTGCCAGCCCTGTCCGTCTTACCCATCCCCAAGCCTA
CTAGAGCAAGAAACCAGTTGTAATATAAAATGCACTGCCACTGTTGGTATGACTACCGTT
ACCTACTGTTGTCAATTGTTATTACAGCTATGCCACTATTATAAGAGCTGTGTAACATCT
CTGGCAAAAAAAAAAAAAA



158/249

FIGURE 156

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68885
><subunit 1 of 1, 432 aa, 1 stop
><MW: 47644, pI: 5.18, NX(S/T): 2
MLQDPDSDQPLNSLDVKPLRKPRIPMETFRKVGIPIIALLSLASIIIVVVLIKVILDKYFY
LCGQPLHFI PRKQLCDGEELDCPLGEDEEHCVKSFP EGP AVAVRLSKDRSTLQV L DSATGNWF
SACFDNFT EAL AETACRQM GYSRAVEIGPDQ DLDV V EITEN S QEL RMRN SSGPCLSGS LVSL
HCLACG KSLKT PRVVG GEEASV DSWP QV SIQYDKQHVC GGSIL DPHW VL TAAHCF RKHT DV
FNWKVRAGSDKLGSF PSLAVAK IIIIEFNPMYPKDNDIALMKLQFPLTFS GTVRPICLPFFD
EELTPATPLWIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPE
GGVDT CQGD SGGPLMYQSDQWHVVGIVSWG YGC GG P STPGV YT KVSAYLNWIYNVWKAEL
```

Transmembrane domain:

amino acids 32-53 (typeII)

**FIGURE 157**

GGGCTGAGGCAC TGAGAGACCGAAAGCCTGGCATTCCAGAGGGAGGGAAACGCAGCGCATCCCCAGGCTCCAG
AGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCCAGCCCTGGGCCTGGACCCCTGGAGCCTCCTGGGC
TTTCCTCTCCAACTGCTTCAGCTGCTGCCGACGACCGGGGGAGGCAGGGCAGGGGCCATGCCA
GGGTCAGATACTATGCAGGGGATGAACGTAGGCACTTAGCTTCTCCACCAGAAGGGCCTCCAGGATTTGACA
CTCTGCTCCTGAGTGGTATGGAAATACTCTACGTGGGGCTCGAGAAGCCATTCTGGCCTTGGATATCCAGG
ATCCAGGGTCCCCAGGCTAAAGAACATGATAACCGTGGCCAGCAGTGACAGAAAAAGAGTGAATGTGCCCTTA
AGAAGAAGAGCAATGAGACACAGTGTTCACCTTCATCCGTGCTGGTTCTTACAATGTCACCCATCTCTACA
CCTGCCGACCTTCGCCCTCAGCCCTGCTTGTACCTTCATTGAACCTCAAGATTCTACCTGTTGCCCATCTCGG
AGGACAAGGTATGGAGGGAAAAGGCCAAGGCCCTTGACCCGCTCACAGCATA CGCTGTCTGGATG
GGATGCTCTATTCTGGTACTATGAACAATTCTCCTGGCAGTGAGCCCATTCTGATGCGCACACTGGATCCAGC
CTGTCCTCAAGACCGACAATTCCCTCCGCTGGCTGCATCATGACGCCCTTTGTGGCAGCCATCCCTCGACCC
AGGTCGCTACTTCTTCAGGGAGACAGCCAGCGAGTTGACTTCTTGAGAGGCTCCACACATCGGGTGG
CTAGAGTCTGCAAGAACATGACGTGGCGGGAAAAGCTGCTGCAGAAGAAGTGGACCACCTCCTGAAGGCCAGC
TGCTCTGCACCCAGCGGGGAGCTGCCCTCAACGTCACTGCCACGCGTCTGCTCCCCGCCATTCTCCA
CAGCTCCCCACATCTACGAGTCTCACCTCCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGGGTTTGTGCCT
TCTCTCTGGACATTGAACGTGTCTTAAGGGAAATACAAAGAGTTGAACAAAGAAACTTCACGCTGGACTA
CTTATAGGGCCCTGAGACCAACCCCGGCCAGGAGCTGCTAGTGGCCCTCCTGTATAAGGCCCTGACCT
TCATGAAGGACCATTCTGATGGATGAGCAAGTGGGGACGCCCTGATGGCACAGCCATTGTCATGTACCTGGGAACCAC
CACGGCTTGCAGTGGAGACAGCCAGGGCCTGATGGCACAGCCATTGTCAGTGGCTCTGGGTTTGTGCCT
GGTCGCTCCACAAGGTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGAAGAGATTCA
CTGCTGTTCCCTGACC
CTGAACCTGTCGAACCTGCAGCTGCCCTGCCAGGGTGAGCTGTTGAGGCTCTCAGGAGGTGTGG
GGGTGCCCGAGCCAAGTGTAGTGTCTATGAGAGCTGTGGACTGTGTCCTGCCGGGACCCACTGTGCCT
GGGACCCCTGAGTCCCGAACCTGTTGCCCTGTCTGCCCTGCCAGGCTGAGCTGTTGAGGCTCTCAGGAGGTGTGG
GGAACCCAGAGTGGCATGTGCCAGTGGCCCTGAGCAGGAGCTGCCAGAGCCGGCAAATCATTA
AAGAAGTCTGGCTGCCCCAACCTCCATCTGGAGCTCCCTGCCAGGCTGAGCTGGCTCTTATTATT
GGAGTCATGGCCAGCAGCAGTCCAGAACGCTCTTCACTGTCTACAATGGCTCCCTTGTGATAGTGCAGG
ATGGAGTTGGGGTCTTACCAAGTGTGGCAACTGAGAATGGCTTTCATACCTGTGATCTCTACTGGTGG
ACAGCCAGGACCAGACCCCTGCCCTGGATCTGAACCTGGCAGGAGCTCCCGGGAGCATGTGAAGGTCCCGTTGA
CCAGGGTCAGTGGTGGGCCCTGGCTGCCAGCAGTCCTACTGCCCTACTTGTCACTGTCACTGTCCT
TTGCCCTAGTGTCTTCAAGGAGCCCTCATCCTCGTGGCTCCCTGGCTGCCAGGCTGAGAGCAG
TTCAGGGCTGTGAGACCCCTGCCCTGGGAGAAGGCCCTGTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGG
AATGCAGGACCTCTGCCAGTGTGGACGCTGACAACAACTGCCCTAGGCAGTAGGACTGAGGTAGCTTAAACTCTAGGCA
CAGGCCGGGCTCGGGTCAGGCACCTGCCAGTGTGGCTGGCGGCCAAGCACAGCCCTGACTAGGATGACAG
CAGCACAAAAGACCACCTTCTCCCTGAGAGGAGCTGTACTCTGCATCACTGATGACACTCAGCAGGGTG
ATGCACAGCAGTGTGCCCTCCCTATGGGACTCCCTTACCAAGCACATGAGCTCTAACAGGGTGGGGCTAC
CCCCAGACCTGCTCCTACACTGATATTGAAGAACCTGGAGAGGATCTCAGTCTGGCCATTCCAGGGACCC
CAGAAACACAGTGTCAAGAGACCCCTAAAAAACCTGCCAGGACCTATGGTAATGAACACCAAACATC
TAAACAACTCATATGCTAACATGCCACTCCTGGAAACTCCACTCTGAAGCTGCCCTGGACACCAACACTCC
TCTCCAGGGTCATGCAGGGATCTGCTCCCTCTGCTTCCCTTACAGTGTGCACCGCTGACTCCAGGAAGTC
TTTCTGAAAGTCTGACCACCTTCTTGTCTCAGTTGGGGCAGACTCTGATCCCTCTGCCCTGGCAGAATGG
CAGGGTAATCTGAGCCTCTTCACTCCTTACCCCTAGCTGACCCCTCACCTCTCCCCCTCCCTTCTTGT
TTTGGGATTCAAGAAAATGCTGTCAGAGACTGTTATTTTATTAAAAATATAAGGCTAAAAAA



160/249

FIGURE 158

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71166
><subunit 1 of 1, 761 aa, 1 stop
><MW: 83574, pI: 6.78, NX(S/T): 4
MALPALGLDPWSLLGLFLFQLLQLLLPTTAGGGGQGPMPRVRYAGDERRALSFFHQKGLQ
DFDTLLLSDGNTLYVGAREAILALDIQDPGVPRLNMIWPWPASDRKKSECAFKKKSNETQC
FNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMEGKGQSPFDPAHKHTA
VLVDGMLYSGTMNNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFVAAPSTQVVYFFE
ETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLPFNVIRHAVLL
PADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKETSRWTTYRGPET
NPRPGSCSVGPSSDKALTFMKDHFILMDEQVVGTPLLVKSGVEYTRLAVETAQGLDGHSHLVM
YLGTTT GSLHKAVVSGDSSAHLVEEIQLFDPPEPVRNLQLAPTQGAVFVGFSGGVWRVPRAN
CSVYESCVDCVLARDPHCAWDPEPESRTCCLLSAPNLNSWKQDMERGNPEWACASGPMSRSLRP
QSRPQIIKEVLAVPNSILELPCPHLSALASYYWSHGPAAVPEASSTVYNGSLLLIVQDGVGG
LYQCWATENGFSYPVISYWVDSQDQLALDPELAGIPREHVKVPLTRVSGGAALAAQQSYWP
HFVTVTVLFALVLSGALIILVASPLRALRARGKVQGCETLRPGEKAPLSREQHLQSPKECRT
SASDVADNNCLGTEVA
```

Signal peptide:

amino acids 1-30

Transmembrane domains:

amino acids 136-156, 222-247, 474-490, 685-704



161/249

FIGURE 159

AGGGTCCCTTAGCCGGCGCAGGGCGCGAGCCCAGGCTGAGATCCGCGGCTCCGTAGAAG
TGAGC**ATG**GCTGGGCAGCGAGTGCTTCTTAGTGGCTTCCTCTCCCTGGGTCTGCTC
TCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACTGATGGA
CCGGGTTCTCAGATTCTCAAGATCACGGTCATAATGTCACCAGCTTAACCACAAAAGAG
GTCCTTTATGCCAGATTAAAAAGAAGAAAATCATATCAAGTTACAGTGGCTTGCA
CCTGAAGATCATCAAAGAGAATTAAAAAGAGTTGATTCTTCTGGAAGAAACTTAGG
TGGCAGAGGAAAATTGAAAACCTATTAAATGTTCTAGAATACTTGGCGTTGCAGTGCAGTC
ATTTTTAAATAGAAAGGATATCATGGATTCTTAAAGAATGAGAACTTCGACATGGTGATA
GTTGAAACTTTGACTACTGTCCTTCCTGATTGCTGAGAAGCTGGGAAGCCATTGTC
CATTCTTCACTCATTGGCTCTTGGATTGGCTACCAATCCCTTGTCTATGTT
CAGTATTCCGTTCTGACTGATCACATGGACTCTGGGCCAGTGAAGAAATTCTG
ATGTTCTTAGTTCTGCAGGAGGCAACAGCACATGCAGTCTACATTGACAACACCATCAA
GGAACATTACAGAAGGCTCTAGGCCAGTTGTCATCTTACTGAAAGCAGAGTTGT
GGTCATAACTCTGACTTTGCTTGATTGCTGACCTCTGCTTCCAACACTGTTAT
GTTGGAGGCTTGATGGAAAAACCTATTAAACCACTGACCAAGACTGGAGAACTTCATTGC
CAAGTTGGGACTCTGGTTTGCTTGACCTGGCTCCATGGTAACACCTGTCAGA
ATCCGAAATCTCAAGGAGATGACAATGCCCTTGCTCACCTACCCAAGGGTGATATGG
AAAGTGTCAAGTGTCTCATTGGCCAAAGATGTCCACCTGGCTGCAAATGTGAAAATTGTTG
CTGGCTTCCCTCAGAGTGACCTCCTGGCTCACCAAGCATCCGTCTGTTGTCACCCACGGCG
GGCAGAATAGCATAATGGAGGCCATCCAGCATGGTGTGCCATGGTGGGATCCCTCTCTT
GGAGACCGCTGAAAACATGGTCCGAGTAGAAGCCAAAAGTTGGTGTCTATTGAGT
AAAGAAGCTCAAGGCAGAGACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGAT
ACAAGTCGGCGGAGTGGCTGCCAGTGTCTGCCTGCGCTCCCACCGCTCAGCCCCACACAG
CGGCTGGGGCTGGATTGACCACTCCTCCAGACAGGGGGCGCAGCAGCTCAAGCCTA
TGTCTTCAGCAGCCCTGGCATGAGCAGTACCTGTCGACGTTTGTGTTCTGCTGGCGT
TCACTCTGGGACTCTATGGCTTTGGAGCTGGAGCTGCTGGCATGGCTGTCTGGTGGCTGCGT
GGGCCAGAAAGGTGAAGGAGAC**TAA**GGCCAGGTGCAGCCTGGCAGGGCTGTGTTGG
GCGATGTCACCATTCTAGGGAGCTCCACTAGTTCTGGCAGCCCCATTCTAGTCCTTC
TAGTTATCTCCTGTTCTGAAGAACAGGAAAATGCCAAAATCATCCTTCCACTTGC
TAATTGGCTACAAATTCATCCTACTAGCTCCTGCCTGCTAGCAGAAATCTTCCAGTCCT
CTTGCCTCCTTGTGCTGCCATCAGCAAGGGCTATGCTGTGATTCTGCTCTGAGTGACTG
GACCACTGACCCCTCAGATTCCAGCCTAAAATCCACCTCCTCTCATGCGCCTCTCGAA
TCACACCCCTGACTCTTCCAGCCTCATGTCAGACCTAGTCAGCCTCTCACTCCTGCC
TACTATCTATCATGGAATAACATCCAAGAAAGACACCTGCAATTCTTCAGTTCTGTT
TGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAGAGTCAGGGC
CGGACACAGGCTCACAGGTCTCCACATTGGTCCCTGTCTGGTCCCCACAGTGAGCTCCT
TCTGGCTGAGCAGGCATGGAGACTGTAGGTTCCAGATTCTGAAAAATAAAAGTTACA
GCGTTATCTCCCCAACCTCACTAA



162/249

FIGURE 160

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71169
><subunit 1 of 1, 523 aa, 1 stop
><MW: 59581, pI: 8.68, NX(S/T): 1
MAGQRVLLLGVFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVMLNHRGP
FMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFFLEETLGGRGKFENLLNVLEYLALQCSHF
LNRKDIDMSLKNENFDMVIVETFDYCPFLIAEKLGKPFVAILSTSFGSLEFGLPIPLSYVPV
FRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHLLKAELWF
INSDFAFDFARPLLPTVYVGGLMEKPIKPVPQDLENFIAKFGDSGFVLVTLGSMVNTCQNP
EIFKEMNNNAFAHLPQGVIWKCQCSHWPKDVHLAANVKIVDWLPQSDLLAHPSIRLFVTHGGQ
NSIMEAIQHGVPVMVGIPLFQDOPENMVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYK
SAAVAASVILRSHPLSPTQRLVGVWIDHVLQTGGATHLKPYVFQQPWHEQYLFDVVFVFLGLT
LGTLWLCGKLLGMMAVWWLRGARKVKET
```

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 483-504



163/249

FIGURE 161

GGGCTGTTGATTTGTGGGGGATTTGAAGAGAGGGAGGAATAGGAGGAAGGGGTTGAGGGGCT
GCCTCTGGCATATGCACACACTCACACATTCTGTACACACCCTCACACACACATACCATGTT
CTCCATCCCCCAGGTCCAGGCCCTAGTGCTGTCCCCTACAGCAGGGCTACCCCTGAAGCTCT
GGCTGCAGCCCTCCCGTCCAGTGGCAGGGGGCTTCATCCCTCTTCTCTCCAAAGCCA
ACTGCTGCACTGCATGCTCTGCCAAGGAGGGAGGAAC TGCACTGCAGTACAGCAGGAGTAAGAGT
GGGAGGCAGGACAGAGCTGGACACAGGTATGGAGAGGGGTTCAGCGAGCCTAGAGAGGGC
AGACTATCAGGGTGCCGGGGT GAGAATCAGGGAGAGGGAGCCAAACAGAACAGAGGGGAGA
AGACCGGGGCACTGTGGGTTGCAGAGCCCTCAGCC **ATGTT**GGGAGCCAAGCCACACTGGC
TACCAAGTCCCCTACACAGTCCCAGGCTGCCCTGGTTCTGGTGCCTCTGCCCTGGGGCC
GGGTGGGCCAGGAGGGGTCAGAGCCCTGCTGGAGGGGAGTGCCTGGTCTGTGA
GCCTGGCCGAGCTGCTGCAGGGGGCCGGGGAGCAGCCCTGGGAGAGGCACCCCTGGC
GAGTGGCATTGCTGCGGTCCGAAGCCACCACATGAGCCAGCAGGGAAACCGGAATGGC
ACCAGTGGGCCATCTACTTCGACCAAGGTCTGGTGAACGAGGGCGGTGGCTTGACCGGGC
CTCTGGCTCCTCGTAGCCCCCTGTCGGGGGTGTCTACAGCTCCGGTCCATGTGGTGAAGG
TGTACAACCGCAAAC TGCCAGGTGAGCCTGATGCTGAACACGTGGCTGTCACTCAGCC
TTGCCAATGATCCTGACGTGACCCGGAGGCAGCCACCAGCTCTGTGCTACTGCCCTGGA
CCCTGGGACCGAGTGTCTCGCCTGCGTCGGGGAAATCTACTGGGTGGTGGAAATACT
CAAGTTCTCTGGCTTCATCTCCCTCTC **TGA**GGACCCAAGTCTTCAAGCACAAGAAT
CCAGCCCTGACAACCTTCTTCTGCCCTCTTGCCCCAGAAACAGCAGAGGCAGGAGAGAG
ACTCCCTCTGGCTCCTATCCCACCTTGCATGGGACCCCTGTGCCAAACACCCAAAGTTAA
GAGAAGAGTAGAGCTGTGCATCTCCAGACCCAGGCCTTCCACCCACCCACCCAGTTAC
CTCCCAGCCACCTGCTGCATCTGTCCTGCAGCCCTAGGATCAGGGCAAGGTTGGCA
AGAAGGAAGATCTGCACTACTTGCCTCTGCTCCTCCGGTTCCCCCAGCTTCC
GCTCAATGCTGATCAGGGACAGGTGGCGCAGGTGAGCCTGACAGGCCCCCACAGGAGCCCAG
ATGGACAAGCCTCAGCGTACCCCTGCAGGCTTCTTCTGTGAGGAAAGCCAGCATCACGGATC
TCAGCCAGCACCGTCAGAAGCTGAGCCAGCACCGTATGGCTAGGGTGGAGGCTCAGCCAC
AGGCAGAAGGGTGGGAAGGGCCTGGAGTCTGTGGCTGGTGAAGGAAGGAAGGAGGGTGTATTG
TCTAGACTGAACATGGTACACATTCTGCATGTATAGCAGAGCAGCCAGCAGGTAGCAATCCT
GGCTGTCCTCTATGCTGGATCCCAGATGGACTCTGGCCCTTACCTCCCCACCTGAGATTAG
GGTAGTGTGTTGCTCTGGCTGAGAGCAGAGCTGAGAGCAGGTATACAGAGCTGGAAAGTGG
ACCATGGAAAACATCGATAACCATGCATCCTCTGCTGGCCACCTCCTGAAACTGCTCCAC
CTTGAAAGTTGAACCTTACTGCCCTCACACTCTGACTGCTGCCTCCTCCAGCTCTC
TCACTGAGTTATCTCACTGTACCTGTTCCAGCATATCCCCACTATCTCTCTTCTCCTGAT
CTGTGCTGTCTTATTCTCCTCTAGGCTTCTATTACCTGGGATTCCATGATTCAATTCTT
CAGACCCCTCCTGCCAGTATGCTAAACCCCTCTCTCTTCTTATCCGCTGTCCATT
GGCCCAGCCTGGATGAATCTATCAATAAAACAACAGAGAATGGTGGTCAGTGAGACACTAT
AGAATTACTAAGGAGAAGATGCCTCTGGAGTTGGATCGGGTGTACAGGTACAAGTAGGTA
TGGTGCAGAGGAAAATAATCAAACGTATACTAAAATTAAAAA



164/249

FIGURE 162

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71180
><subunit 1 of 1, 205 aa, 1 stop
><MW: 21521, pI: 7.07, NX(S/T): 1
MLGAKPHWLPGPLHSPGLPLVLVLLALGAGWAQEGSEPVILLEGECLVVCEPGRAAAGGPGGA
ALGEAPPGRVAFAAVRSHHHEPAGETGNGTSGAIYFDQVLVNEGGGFDRASGSFVAPVRGVY
SFRFHVVKVYNRQTVQVSLMLNTWPVISAFAANDPDVTREAATSSVLLPLDPGDRVSLRLRRG
NLLGGWKYSSFSGFLIFPL
```

Signal peptide:

amino acids 1-32



U.S. PATENT & TRADEMARK OFFICE

165/249

FIGURE 163

GCTGTTCTCTCGGCCACCACTGGCCGGCCGCAGCTCCAGGTGTCCTAGCCGCCAGC
CTCGACGCCGTCCGGGACCCCTGTGCTCTGCGGAAGCCCTGGCCCCGGGGCCGGGCAT
GGGCCAGGGCGGGGTGAAGCGGCTTCCCGGGCCGTGACTGGCGGGCTTCAGCC**AT**
GAAGACCTCATAGCGCCTACTCCGGGTCTGCGCGAGCGTCAGGCCGAGGCTGACC
GGAGCCAGCGCTCTCACGGAGGACCTGCGCTGCGCGAGGGGTCTGGAGATGGGGCACT
GGATCCAGCATTCTCCGCCCTCCAGGACCTTTCTGTACCTGGCTCAATAGGTCAA
GGTGGAAAAGCAGCTACAGGTATCTCAGTGTCCAGTGGCTGTCCCTGTACTGG
GAGTGGCCTGCAGTGCCATCCTCATGTACATATTCTGCACTGATTGCTGGCTATCGCTGTG
CTCTACTTCACTGGCTGGTGTGACTGGAACACACCCAAGAAAGGTGGCAGGAGGTACA
GTGGGTCCGAAACTGGCTGTGTCAGGACTACTTCCCATCCAGCTGGTA
AGACACACAAACCTGCTGACCACCAGGAACCTATATCTTGATACCACCCCCATGGTATCATG
GCCCTGGGTGCCTCTGCAACTTCAGCACAGAGGCCACAGAAGTGA
CATACGGCCTTACCTGGCTACACTGGCAGGCAACTCCGAATGCCTGTGTTGAGGGAGTACC
TGATGTCTGGAGGTATCTGCCCTGTCAGCCGGACACCATAGACTATTGCTTCAAAGAAT
GGGAGTGGCAATGCTATCATCATCGTGGTGGGGTGCAGGCTGAGTCTCTGAGCTCCATGCC
TGGCAAGAATGCAGTCACCTGCGGAACCGCAAGGGCTTGTGAAACTGGCCCTGCGTCATG
GAGCTGACCTGGTCCCCTACTCCTTGAGAGAATGAAGTGTACAAGCAGGTGATCTC
GAGGAGGGCTCCTGGGCGATGGGTCCAGAAGAAGTCCAGAAATACATTGGTTGCC
ATGCATCTTCCATGGTCAGGCCTCTCCTCCGACACCTGGGGCTGGTGCCTACTCCA
AGCCCCATCACCACGTGGGAGAGGCCATCACCACCCAGCTGGAGCACCCACCCAG
CAAGACATCGACCTGTACCATGTACATGGAGGCCCTGGTGAAGCTTCGACAAGCA
CAAGACCAAGTCCGGCTCCGGAGACTGAGGTCCGGAGGTGAAC**TGA**GCCAGCCTCGGG
GCCAATTCCCTGGAGGAACCAGCTGCAAATCACTTTTGCTGTAAATTGGAAGTGTCA
TGGGTGTCTGTGGTTATTAAAAAGAAATTATAACAATTGCTAAACCAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAA



166/249

FIGURE 164

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71184
><subunit 1 of 1, 388 aa, 1 stop
><MW: 43831, pI: 9.64, NX(S/T): 3
MKTLIAAYSGVLRGERQAEADRSQRSHGGPALSREGSGRWGTGSSILSALQDLFSVTWLNR
KVEKQLQVISVLQWVLSPFLVIGVACSAILMYIFCTDCWLIAVLYFTWLVDWNTPKKGRRS
QWVRNWAVWRYFRDYFPIQLVKTHNLLTRNYIFGYHPHGIMGLGAFCNSTEATEVSKKFP
GIRPYLATLAGNFRMPVLREYLMGGICPVSRTIDYLLSKNGSGNAIIVVGAAESLSSM
PGKNAVTLRNRKGFKLALRHGADLVPIYSFGENEVYKQVIFEEGSWGRWVQKKFQKYIGFA
PCIFHGRGLFSSDTWGLVPYSKPITTVVGEPIТИPKLEHPTQQDIDLYHTMYMEALVKLFDK
HKTGFGLPETEVLEVN
```

Important features of the protein:

Transmembrane domain:

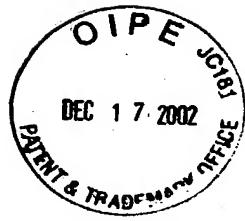
amino acids 76-97

N-glycosylation sites.

amino acids 60-63, 173-176, 228-231

N-myristoylation sites.

amino acids 10-15, 41-46, 84-89, 120-125, 169-174, 229-234, 240-245, 318-323, 378-383



167/249

FIGURE 165

GGGCGGCGGGATGGGGCCGGGGCGGCCGCGCACTCGCTGAGGCCCGACGCAGGGCCGGCCGGGCCA
GGGCGAGGAGCGCGCGGCCAGAGCAGGGCGCGAGGCAGGCCGGACGCCGCGACGAGCAGGTGGCG
GCGGCTGCAGGCTTGTCCAGCCGAAGCCCTGAGGGCAGCTGTCCCCTGGCTCTGCTGACCTGTGCCTTGA
CGCTGTCCTCAGCGAGGGCCGTGCACCCGCTCTGAGCAGGCCATGGCCTGCTGGCCTCTGAAGACCCA
GTCGTGCTGCACCTGCTGGCTGGCTTGCTTCGTGGTAGTGGCTGGTCAACTCGTCCAGCTGTGCAC
GCTGGCGCTGGCCGGTCAGCAAGCAGCTACCGCCCTCAACTGCCCTCGCTACTCACTCTGGAGCCA
ACTGGCATGCTGGAGTGGTAGTGGCTGCACGGAGTGTACACTGTTACCGGACCAGGCCACGGTAGAGCGCTT
TGGGAAGGAGCACGAGTCATCATCCTCAACCACAACCTCGAGATCGACTCCTCTGTGGTAGGACATGTGA
GCGCTCGGAGTGTGGAGCTCCAAGGCCTCGCTAAGAAGGAGCTGCTTACGTGCCCTCATCGGCTGGAC
GTGGTACTTCTGGAGATTGTGTTCTGCAAGCGGAAGTGGAGGAGGACCGGGACACCGTGGTGAAGGGCTGAG
GCGCCTGTCGGACTACCCGAGTACATGTGGTTCTCCTGTACTCGAGGGACGCCACGGAGACCAAGCA
CCCGCTTAGCATGGAGGTGGCGCTGCTAAGGGCTCCCTGCTCAAGTACCGCCCTGCGCCGGACCAAGGG
CTTCACCACCGCAGTCAGTCAGTCCTCCGGGACAGTCAGCTGTATGATGTAACCTGAACCTCAGAGGAAA
CAAGAACCGTCCCTGCTGGGATCCTCTACGGGAAGAAGTACCGAGGCGACATGTGCGTAGGGAGATTCCCTCT
GGAAGACATCCCCTGGATGAAAAGGAAGCAGCTCAGTGGCTTCATAAAACTGTACCGAGAGAAGGACGCGCTCCA
GGAGATATATAATCAGAAGGGCATGTTCCAGGGAGCAGTTAACGCTGCCGGAGGCCGTGGACCCCTCTGAA
CTTCCTGTCCTGGGCCACCATTCTCCTGTCTCCCTCTCAGTTGTCTGGCGTCTTGCCAGCGGATCACC
TCTCCTGATCCTGACTTCTTGGGTTGTGGAGCAGCTCCTTGGAGTTCGCAGACTGATAGGAGAATCGCT
TGAACCTGGAGGTGGAGATTGCATGAGCTGAGATGGCATCACTGTACTCCAGCCTAGGCAACAGAGCAAGACT
CAGTCTAAAAAAAAAAAAACAAAAACCCCCAGAAATTCTGGAGTTGAACTGTGAGTTACTGACATGAAAA
ATTCACTAGAGGCTGAACAGCAGATTGAGCAGGAGAAAAATCAGCAAGCTGAAGATGGTACCTTGAGATT
TTTCAGGCTAATGAAAAAGAATGAAGGAAAATTACAGCCTCAGAGACCCATGGTGCACCGTCACACAAATCAA
CATATGCATGATGAGAGTCCCAGAAGGAGAGGAGAAAGGGTCAGAAAGAATGCCACAAGCTGATGAAAAACA
GTAACCTACCCACTCAGGAAGCTCAGTGAACTCCAATGAGGATGAATATCAGAGATCCACACCTAGATATTCAT
AATCAAAGTGTCAAATGACAAAGAATCTGAAAGCAGCAAGAGATGAGCAACTTATCTTGTCAAAGGATCTTG
ATCAGATTAACAGCTCATTCCTCAGAAATCATGGAGGCCAGGAGATAGTGGATGAAACACTGTTGAAGGCAA
AACCTCAACTGTAATTATTGGACTTTGAGCTTAGATGGCTTGACCTCTTGCTTCAGGGACAGTTTCA
ATTTAATCCCTAATAACAATTAGTCAAGCTCCTTGACCTGTAGGAAGGCCGTGTCTTAGGCCGGCACAGTGGC
TTACACCTGTAATCCAGCACTTGGGAGGCCAGACGGGTGGATCATTGGGTCAAGCTGATCTCAAACCTCCT
GAGTTAGGTGATGCTGCTTATTGCCATTGTATATCTTCTATCTTGGGAAATGTCTGTTCAAGTCCCTTG
CCTTTAAATTATTATTATTATTATTATTGAGACAGGGCTTGTGTTGCTGCCAGGCTGGAGTA
CAGTGGCACAGTCTGGCTCACTGCAGCCTCGACCTCCTGGCTGAGCTGATCCTCCACCTCAGCCTCCCTGT
AGCTGTATTGGTATTGTAGCTGTAGTTGTATTGTGTTGAGACAGGGCTGGAGACAGCATTCAACCATGA
TGCCCAGGCTGGCTTGAACCTGAGCTCAAGTGTGATCTGCCCTGCTCAGCCTCCAAAGTGTGGATTACAGA
CATGAGCCACTGCACCTGGCAAACCTCCAAAATTCAACACACACACACACACACACACACACACACACACAC
GAGGGGCCGGGTGTGGCCCAACTACCAGGGAGACTGAAGTGGAGGATCGCTGGCATGAGAAGTCGAGGCTG
CAGTGAGTCGAGGTTGTGCGACTGCATTCCAGCCTGGACAACAGAGTGAGACCCCTGTCTC



168/249

FIGURE 166

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71213
><subunit 1 of 1, 368 aa, 1 stop
><MW: 42550, pI: 9.11, NX(S/T): 1
MGLLAFLKTQFVLHLLVGFVFVVSGLVINFVQLCTLALWPVSKQLYRRLNCRLAYSLWSQLV
MLLEWWSCTECTLFTDQATVERFGKEHAVIILHNFEIDFLCGWTMCERFGVLGSSKVLAKK
ELLYVPLIGWTWYFLEIVFCKRKWEEDRDTVVEGLRRLSDYPEYMWFLLYCEGTRFTETKHR
VSMEVAAAKGLPVLYHLLPRTKGFTTAVKCLRGTVAAVYDVTLNFRGNKNPSLLGILYGGKK
YEADMCSVRRFPLEDIPLDEKEAAQWLHKLYQEKDALQEIYNQKGMFPGEQFKPARRPWTLLN
FLSWATILLSPLFSFVLGVFASGSPLLILTFLGFVGAASFGVRRRLIGESLEPGRWRLQ
```

Important features of the protein:

Signal peptide:

amino acids 1-25

Transmembrane domains:

amino acids 307-323, 335-352

Tyrosine kinase phosphorylation sites.

amino acids 160-168, 161-169



169/249

FIGURE 167

GATATTCTTATTTAAGAACCTGAAGTACTATGCATCACTCCCTCCAATGTCCTGGGGCA
GCCACCAGGCATATTCATCTTGTGTGTTTCTTGCTTAGCACTGGGGCACTTCTT
GCTTATTCTTGTTAGGAAAGGGCTCAGTTGTCTGTTGGGGTGGCAGGCAGGCCG
GCTTACGCCCTGATAACGCCCTGGGTAGAAGGGAAGGGAAAGATAAACTTTATACAAATGGG
GATAGCTGGGTCTGAGACCTGCTCCTCAGTAAAATTCTGGGATCTGCCTATACCTCTT
TTCTCTAACCTGGCATACCCCTGCTAAAGCCTCTCAGGGCTCTCTCTGTTCTAGGATCAA
AGTATTTAGAGCTACAAGAGCCCTCATGGTCTGCCCTGCCCTGGCCAGCTTCATTGT
ACATGTGGTGTCTTGCGTTCTGTATAATGTGGTATGCCATGGGTCTTGCACAAGCCT
TTCCTCTTGCTGGACACTGTTCCCTGCCCTGGGACTACTCTTCCTACTTAATATGTAGTC
ATCCTGCAGATTCAATTCTAACATCATTCTCCAGGGATCCTGGCCTGACAGAAATCTCAT
CTTGTAAATGCTCTCATAAGACCACTGTTCCCTTGCAGCACTGCCACTCAGTTGA
TCTTATGTGCGTTGTGGTTGTATGGTTGTCTGTTCCCCAGAATGCCAGCTGAGC
TGCCTGAGGGTCAAGGGCATTGCTGTGCCCTGCCAGGTATAGCCTACATGTGGTGGTGCT
CATGTTTAGAGACTAAATGGAGGAGGAGATGAGGAAAAGATTGAAATCTCAGTTCACCA
GATGGTAGGGCCCAGCATTGAAATTCACACGTTGACTGTGCTGTGAATTATCTGGGA
TGCAGGTCTGATTCACTAGTGGCCAGGTTGGCATCTCTAACAAACTCCCACGTGATGCTGA
TGCTGGCCTATGAACCTACTAAATAGTAAGAACATCTATGGAGCCAGGCTGGCATGGTGGC
TCACACCTATGATCCCAGCACTTGGGAGGCTGAGGCAGGCTGATCACCTGGAGTCAGGATT
TCAAGACTAGCCTGGCAACATGGTGGAACCCATCTGTACTAAAAACACAAATTAGCTG
GGCATGGTGGCACATGCCGTAGTCCCAGCTACTTGGGAGGCTGAAGCAAGAGAATCGCTTG
AACCTGGGAGGCGGAGGTTGCAGTGAGCCGAGATCAGGCCACTGTATTCCAACCAGGGTGAC
AGAGTGAGACTCTATGTCAAAAAAAAAAAAAAA



170/249

FIGURE 168

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71234  
><subunit 1 of 1, 143 aa, 1 stop  
><MW: 15624, pI: 9.58, NX(S/T): 0  
MHSLQCPGAATRHIHLCVCF$FALALGHFLLISLVGKGLS$LCGVGGRQAGLRLIRPWRR  
EGKINFYTNGDSWGLRPASSVKFLGSAYTFFSLTWHTLLKASQGFSLFLGSKYLELQEWS  
GPCPPGQLHCTCGVLLSFL
```

Important features of the protein:

Signal peptide:

amino acids 1-28



171/249

FIGURE 169

GGCTGGACTGGAACCTCCTGGTCCAAGTGATCCACCCGCCTCAGCCTCCCAAGGTGCTGTGA
TTATAGGTGTAAGCCACCGTGTCTGGCCTCTGAACAACTTTTCAGCAACTAAAAAGCCAC
AGGAGTTGAACTGCTAGGATTCTGACT**ATG**CTGTGGCTAGTGCTCCTACTCCTACCTAC
ATTAAAATCTGTTTTGTTCTTGTAACTAGCCTTACCTCCTAACACAGAGGATCTGT
CACTGTGGCTCTGCCCAAACCTGACCTTCACTCTGGAACGAGAACAGAGGTTCTACCCAC
ACCGTCCCCCTCGAAGCCGGGACAGCCTCACCTGCTGGCCTCTCGCTGGAGCAGTGCCCTC
ACCAACTGTCTCACGTCTGGAGGCAGTGACTCGGGCAGTGCAGGTAGCTGAGCCTCTGGTA
GCTGCGGCTTCAAGGTGGCCTTGCCTGGCGTAGAAGGGAT**TGA**CAAGCCGAAGATT
CATAGGCGATGGCTCCACTGCCAGGCATCAGCCTGCTGTAGTCATCACTGCCCTGGGG
CCAGGACGGGCCGTGGACACCTGCTCAGAAGCAGTGGTGAGACATCACGCTGCCGCCAT
CTAACCTTTATGTCCTGCACATCACCTGATCCATGGCTAATCTGAACCTGTCCCAAGG
AACCCAGAGCTTGAGTGAGCTGTGGCTCAGACCCAGAAGGGGTCTGCTTAGACACCACCTGGTT
TATGTGACAGGACTTGCATTCTCCTGGAACATGAGGGAACGCCGGAGGAAAGCAAAGTGGCA
GGGAAGGAACTTGTGCCAATTATGGGTAGAAAAGATGGAGGTGTTGGTTATCACAAGGC
ATCGAGTCTCCTGCATTCACTGGACATGTGGGGGAAGGGCTGCCATGGCGATGACACACT
CGGGACTCACCTCTGGGCCATCAGACAGCCGTTCCGCCCGATCCACGTACCAGCTGCTG
AAGGGCAACTGCAGGCCGATGCTCTCATCAGCCAGGCAGCAGCAGCAGCAGCAGCAG
CCAGGGCAGCCGTCTGGGAAGGAGCAAGCAAAGTGACCATTCTCCTCCCTCCCTC
TGAGAGGCCCTCCTATGTCCTACTAAAGCACCAGCAAGACATAGCTGACAGGGCTAATG
GCTCAGTGTGGCCCAGGAGGTAGCAAGGCCTGAGAGCTGATCAGAAGGCCTGCTGTGCG
AACACGGAAATGCCCTCAGTAAGCACAGGCTGAAAATCCCCAGGCAAAGGACTGTGTGGCT
CAATTAAATCATGTTCTAGTAATTGGAGCTGTCCCCAAGACCAAAGGAGCTAGAGCTTGGT
TCAAATGATCTCCAAGGGCCCTTATAACCCAGGAGACTTGATTTGAATTGAAACCCAAA
TCCAAACCTAAGAACCCAGGTGCATTAAGAACATCAGTTATTGCCGGGTGTTGGCCTGTAATG
CCAACATTTGGGAGGCCAGGCAGGCTAGATCACCTGAGGTAGGAGTTCAAGACCCAGCCTG
GCCAACATGGTGAACCCCTGTCTACTAAAAAATACAAAAAAACTAGCCAGGCATGGTGGT
GTGTGCCTGTATCCCAGCTACTCGGGAGGCTGAGACAGGAGAATTACTTGAACCTGGGAGGT
GAAGGAGGCTGAGACAGGAGAATCACTTCAGCCTGAGCAACACAGCGAGACTCTGTCTCAGA
AAAAATAAAAAAGAATTATGGTTATTTGTAA



172/249

FIGURE 170

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71277

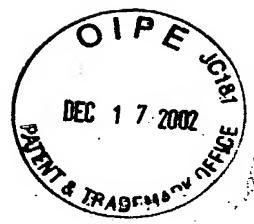
><subunit 1 of 1, 109 aa, 1 stop

><MW: 11822, pI: 8.63, NX(S/T): 0

MLWWLVLLLLPTLKSVFCSLVTSLYLPNTEDLSLWLWPKPDLHSGTRTEVSTHTVPSKPGTA
SPCWPLAGAVPSPTVSRLEALTRAVQVAEPLGSCGFQGGPCPGRRD

Signal peptide:

amino acids 1-15



173/249

FIGURE 171

GCGGGCCCGCGAGTCCGAGACCTGTCCCAGGAGCTCCAGCTCACGTGACCTGTCACTGCCTC
CCGCCGCCCTCCTGCCCGGCCATGACCCAGCCGGTCCCCGGCTCTCCGTGCCGCCGCC
GGCCCTGGGCTCAGCCGACTGGCGCCCTCGCCACTGGCCTCTCCTGGGGAGGGCGGT
GCCCCCCATGGCGAGGCCGGCGAGAGCAGTCGCTGCTCCCCCGAGGACAGCCGCTGTGG
CAGTATCTTCTGAGCCGCTCCATGGGGAGCACCCGGCGTGCAGCAGCTGAGGCTGCTGAC
CCTGGAGCAGCCGCAGGGGATTCTATGATGACCTGCGAGCAGGCCAGCTCTGCCAAC
TGGCGCGGCTCATCCAGGCCAAGAAGGCCTGGACCTGGCACCTCACGGCTACTCCGCC
CTGGCCCTGGCCCTGGCGCTGCCCGGGACGGCGCGTGGTACCTGCGAGGTGGACCGCA
GCCCGGAGCTGGACGGCCCTGTGGAGGCAGGCCAGGCCAGCACAGATGACCTCC
GGCTGAAGCCCGCCTGGAGACCCCTGGACGAGCTGCTGGCGGGCGAGGCCGACCTTC
GACGTGGCGTGGATGCGGACAAGGAGAACTGCTCCGCCTACTACGAGCGCTGCCTGCA
GCTGCTGCGACCCGGAGGGCATCCTCGCCGTCCCTCAGAGTCCTGTGGCGGGAGGTGCTGC
AACCTCCGAAAGGGGACGTGGCGGCCGAGTGTGCGAACCTAAACGAACGCATCCGGCG
GACGTCAAGGTCTACATCAGCCTCCTGCCCTGGCGATGGACTCACCTGGCCTCAAGAT
CTAGGGCTGGCCCTAGTGAGTGGCTCGAGGGAGGGTTGCCTGGGAACCCCAGGAATTGAC
CCTGAGTTTAAATCGAAAATAAGTGGGCTGGACACAAAAAAAAAAAAAA



174/249

FIGURE 172

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71282
><subunit 1 of 1, 262 aa, 1 stop
><MW: 28809, pI: 8.80, NX(S/T): 1
MTQPVPRLSVPAALALGSAALGAAFATGLFLGRRCPWGRGRREQCLLPPEDSRLWQYLLSRS
MREHPALRSLRLLTLEQPQGDMSMTCEQAQLLANLARLIQAKKALDLGTFTGYSALALALAL
PADGRVVTCEVDAQPPELGRPLWRQAEAEHKIDLRLKPALETLDELLAAGEAGTFDVAVVDA
DKENCSAYYERCLQLLRPGGILAVRLVLWRGKVLQPPKGDVAAECVRNLNERIRRDVRYI
LLPLGDGLTLAFKI
```

Important features of the protein:

Signal peptide:

amino acids 1-25

Transmembrane domains:

amino acids 8-30, 109-130

N-glycosylation site.

amino acids 190-193

Tyrosine kinase phosphorylation site.

amino acids 238-246

N-myristoylation sites.

amino acids 22-27, 28-33, 110-115, 205-210, 255-260

Amidation sites.

amino acids 31-34, 39-42



175/249

FIGURE 173

CCGCCGCCAGCCGCTACCGCCGCTGCAGCCGTTCCGGCCTGGGCCTCTGCCGTCA
GCATGCCACACGCCCTCAAGCCGGGACTGGTGTGCTAAGATGAAGGGCTACCCCTCAC
TGGCCTGCCAGGATCGACGACATCGGGATGGCCGTGAAGCCCCACCAACAAGTACCC
CATCTTTCTTGGCACACACGAAACAGCCTCTGGACCCAAGGACCTGTCCCCCTACG
ACAAATGTAAAGACAAGTACGGGAAGCCAACAAGAGGAAAGGCTCAATGAAGGGCTGTGG
GAGATCCAGAACACCCCCACGCCAGCTACAGGCCCTCCGAGTGTGAGCTCTCCGACAG
CGAGGCCCGAGGCCAACCCGCCAGGGCAGTGAAGCTGACGCCAGGACATGAGGACCGGG
GGGTATGCCGTACAGCGTAACCGCCACAGCTGCCAGCAGGATGGAGAGCGACTCA
GAUTCAGACAAGAGTAGCGACAACAGTGGCTGAAGAGGAAGACGCCCTGCCTAAAGATGTC
GGTCTCGAAACGAGCCCAGAGGCTCCAGCGACCTGGATCAGGCCAGCGTGTCCCCATCCG
AAGAGGAGAACTCGAAAGACTCATCTGAGTCGGAGAAGACCGACAGGACTCACACCT
GAGAAGAAAGCAGCGTCCGGGCCACGGAGGGCCCTCTGGGGGGACGGAAAAAAAGAA
GGCGCCGTCAAGCCTCCGACTCCGACTCCAAGGCCATTGGACGGGCCAAGCCTGAGCCGG
TGGCCATGGCGCGGTCCGGCTCTCCTCTCTCTCTCCCTCCGACTCCGATGTG
TCTGTGAAGAACGCTCCGAGGGGCAGGAAGCCAGCGAGAAGCCTCTCCGAAGCCGCGAGG
GCGGAAACCGAACGCTGAACGGCCTCCGTCCAGCTCCAGCAGTGAAGCTGACAGCGACGAGG
TGGACCGCATCAGTGAGTGGAGCAGGAGGAGCTCGGGCCTCGGGAGCAGGAGAAGGAGGAGAAGGA
CGGGAGGCCGAGCAGGCCGACCAGGGAGGCTGAGCGGGCAGCAGCGAGCTGGAGGCGGG
ACGAGCTCAGGGAGGAGCATGAGCCGTCAAGAACGGGGACGCAAGGGCCGGGGCGGG
CCCCCGTCTCTCTGACTCCGAGCCCGAGGCCAGCTGGAGAGAGAGGCCAAGAAATCAGC
GAAGAACGCCAGTCCTCAAGCACAGAGCCGCCAGGAAACCTGGCCAGAAGGAGAAGAGAG
TGCAGGCCAGGGAGGAAGCAACAAGCCAAGCCGTGAAGGTGGAGCGGACCCGAAGCGGTCC
GAGGGCTCTCGATGGACAGGAAGGTAGAGAAGAAGAAAGGCCCTCGTGGAGGGAGAAGCT
GCAGAACGCTGCACAGTGAGATCAAGTTGCCCTAAAGGTGACAGCCGGACGTGAAGAGGT
GCCTGAATGCCCTAGAGGAGCTGGGAACCCCTGCAGGTGACCTCTCAGATCCTCAGAAC
ACAGACGTGGTGGCCACCTTGAAGAAGATTGCCGTACAAAGCGAACAGGACGTAATGGA
GAAGGCAGCAGAACGCTATAACCGGCTCAAGTCGCCCTCGGAGGCCAAAGATCGAGGCCG
TGCAGAACAGTGAACAAGGCTGGGATGGAGAAGGAGAAGGCCAGGAGAAGCTGGCCGGGAG
GAGCTGGCCGGGAGGAGGCCAGGAGAAGGCCAGGAGAAGGCCAGCACCAGTCTCTC
AGCCCGAGTGAATGGCGAGGCCACATCACAGAACGGGGAGAGCGCAGAGGACAAGGAGCACG
AGGAGGGTCGGGACTCGGAGGAGGGCCAAGGTGTGGCTCTGAAGACCTGCACGACAGC
GTACGGGAGGGTCCGACCTGGACAGGCCCTGGAGCGACGGAGGAGAGCTGA
GGGGGACTCGGAGGCCCTGGAGAGAGCT**TGA**GCCGCCAGGCCAGGCCAGCCCCCGC
CCGAGCTCAGGCTGCCCTCTCCTCCCCGGCTCGCAGGAGAGCAGAGCAGAGAACTGTGGG
GAACGCTGTGCTTTGTATTGTCCCTGGTTTTTCTGCCTAATTCTGTGATT
TCCAACCAACATGAAATGACTATAACGGTTTTAATGA



176/249

FIGURE 174

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71286
><subunit 1 of 1, 671 aa, 1 stop
><MW: 74317, pI: 7.61, NX(S/T): 0
MPHAFKPGDLVFAKMKGYPHWPARIDDIADGAVKPPPNKYPIFFFGTHTAFLGPKDLFPYD
KCKDKYGKPNKRKGFNEGLWEIQNNPHASYSAPPVSSSDSEAPEANPADGSDADEDDERG
VMAVTAVTATAASDRMESDSDSDKSSDNGLRKTPALKMSVSKRARKASSLDQASVPSE
EENSESSSESEKTSDQDFTPEKKAAVRAPRRGPLGGRKKKAPSASDSDSKADSDGAKPEPV
AMARSASSSSSSSSSDSVVKPPRGRKPAEKPLPKPRGRKPAPPERPPSSSSDSDEVS
DRISEWKRREARRRELEARRREQEEELRRLREQEKEEKERRERADRGEAERGSGGSSGD
ELREDDEPVKKRGRKGRGRGPPSSSDSEPEAELEREAKKSACKPQSSSTE PARKPGQKEKRV
RPEEKQQAKPVKVERTRKSEGFSDRKVEKKKEPSVEEKLQKLHSEIKFALKVDSPDVKRC
LNALEELGTLQVTSQILQKNTDVVATLKKIRRYKANKDVMEEAAEVYTRLKSRLGPKIEAV
QKVNKAGMEKEKAEEKLAGEELAGEEAPQEKAEDKPSTDLSAPVNGEATSQKGESAEDKEHE
EGRDSEEGPRCGSSEDLHDSVREGPDLDLDRPGSDRQERERARGDSEALDEES
```

Signal peptide:

amino acids 1-13



100 101 102 103 104 105 106 107 108

177/249

FIGURE 175

GTGGTTCTCCTGGATCTCACCTACCAACTGCAGATCTGGGACTCATCAGCCTCAATAATTATTAATTAAATTA
ACACCATTGAAAGAGAACATTGTTTCATCATGAATGCTAATAAGATGAAAGACTTAAAGCCAGAACCCAAGA
TTTCACCTTTCTGTTGATGATGCTAACGATGACCATGTTCTCAAATAGCTGTATCCCTTTGGGTTCATC
AAATATTCCAAGACTCAAGCTAACCTACAAAGACTTGCTGTTCAAATAGCTGTATCCCTTTGGGTTCATC
AGAAGGACTGGATTTCAAACTCTCTCTTAGATGAGGAAGAGGCCAGGCTGCTTGGGAGCCAAAGACCACAT
CTTCTACTCAGTCTGGTACTAAACAAAATTAAAGAGATGAAAGACTTATTGGGCTGCTGCAAAGGAACGGGTTGA
ATTATGTAATTAGCTGGAAAGATGCAACACAGAATGTCATACTCAGAGTACTTCAGCCCTATAACAA
AACTCACATATAATGTGTGGAACCTGGAGCATTCATCCAATATGTGGGTATATTGATCTGGAGTCTACAAGGA
GGATATTATATTCAAACAGACACACATAATTGGAGTCTGGCAGACTGAAATGTCCTTCGATCCTCAGCAGCC
TTGCTTCAGTAATGACAGATGAGTACCTCTACTCTGGAACAGCTCTGATTTCCTGGCAAAGATACTGCATT
CACTCGATCCCTGGGCCTACTCATGACCACACTACAGAACTGACATTTCAGAGCACTACTGGCTCAATGG
ACAAAATTATTGAAACTTCTCATACCAAGACACCTACAATCCAGATGATGATAAAATATTTCTTCTTCG
TGAATCATCTCAAGAAGGCAGTACCTCGATAAAACCATCCTTCGAGTTGGAGAGTTGTAAGAATGATGT
AGGAGGACAACGCAGCCTGATAAAACAAGTGGACGACTTTCTTAAGGCCAGACTGATTGCTCAATTCTGGAAG
TGATGGGGCAGATACTTACTTGATGAGCTCAAGATATTATTACTCCCCACAAGAGATGAAAGAAATCTGT
AGTATATGGAGTCTTACTACAACCAGCTCCATCTCAAAGGCTCTGCTGTTGTGATAGCATGGCTGACAT
CAGAGCAGTTTAATGGTCCATATGCTCATAGGAAAGTGCAGACCCTGTTGGGTGCACTGATGAGGAGAAT
TCCTTATCCACGGCCTGGTACATGTCCAAGCAAAACCTATGACCCACTGATTAAGTCCACCCGAGATTTCAGA
TGATGTCATCAGTTCTAAAGCGGCACTCTGTGATGTATAAGTCCGTATACCCAGTTCGAGGAGGACAAACGTT
CAAGAGAATCAATGTGGATTACAGACAGATGACACAGATGTTGAGCATGTCATTGAGAAGATGGCAGTACGA
TGTAAATGTTCTGGAACAGACATTGGAACCTGCTCAAAGTTGTCAGCATTCAGGAAATGTCCTGAAAGCA
AGAGGTAGTGCCTGGAGGAGTTGAGATATTCAAGCACTCATCAATCATCTGAACTGGAAATTGTCCTGAAAGCA
GCAACAAATTGTACATTGGTCTCCGAGATGAGATTAGTTCAGCTCTCTGACAGATGCGACACTATGGAAAGC
TTGCGCAGACTGTTCTTGCCAGAGACCCCTACTGCGCTGGATGGAATGCATGCTCTCGATATGCTCCTAC
TTCTAAAAGGAGAGCTAGACGCCAAGATGTAATGGCACCACATCACCAGTGTGCTGGACATCGAAGACAG
CATTAGTCATGAAACTGCTGATGAAAAGGTGATTTGGCATTGAAATTAACTCAACCTTCTGGAATGTATACC
TAAATCCAAACAAGCAACTATTAAATGGTATATCCAGAGGTCAAGGGATGAGCATGAGAGGAGTTGAAAGCCCAGA
TGAAAGAATCATCAAAACGGAATATGGCTACTGATTGCAAGTTGCAAGAAGAAGGATTCTGGATGATTACTG
CAAAGCCCAGGAGCACACTTCATCCACACCATACTGAAAGCTGACTTTGAATGTCATGAGAATGAACAGATGGA
AAATACCCAGAGGGCAGAGCATGAGGAGGGCAGGTCAGGATCTATTGGCTGAGTCACGGTTGAGATACAAAGA
CTACATCCAAATCTTAGCAGCCAAACTCAGCTCGAGGACTCTGCAACAGATGTCAGGAGAAGCG
GAGACAGAAGAACAGGGGGCCCAAAGTGGAAAGCACATGCAAGGAAATGAAGAAGAACAGAAATCGAAGACATCA
CAGAGACCTGGATGAGCTCCCTAGAGCTGAGCCACCTGTTCTACTTAATTAAAGAAAAGAATTCCCTTAC
TATAAAACATTGCCCCCTGTTGATATCCCTTATAGTAATTCAAAATGCTTCCATGGAGTTTGCTAAGG
CACAAGACAATAATCTGAATAAGACAATATGTGATGAAATATAAGAAAGGCAAAATTCAATTGAAACCAGTTT
CCAAGAACAAATCTGCACAAGCAAAGTATAAGAATTATCTAAAAATAGGGGTTTACAGTTGAAATGTTTA
TGTTTGAGTTGGATTATGTGATGAAATAGTGTGAGCTAAGCAAGCCCCGAATTGATAGTGTATAAGGT
GCTTATTCCCTCGAATGTCCATTAAGCATGGAATTACCATGCGAGTTGTGCTATGTTCTATGAACAGATAT
CATTCTATTGAGAACAGCTACCTTGTGGTAGGAAATAAGAGGTCAAGACACAAATTAAAGACAACCTCCATTATC
AACAGGAACCTTCTCAGTGAGCCATTCACTCCTGGAGAATGGTATAGGAATTGGAGAGGTGCATTATTTCTTC
TGGCCACTGGGGTTAAATTAGTGTACTACAACATTGATTACTGAGGGCACTAATGTTCCCCCAGGATTCT
ATTGACTAGTCAGGAGTAACAGGTTCACAGAGAGAATTGGTGTGCTTAGTTATGTGTTTTAGAGTATATACTAA
GCTCTACAGGGACAGAATGCTTAATAAAATCTTAATAAGATAAGGAAAATTAAATAAAACAAGGAAAACA
TAATGATGATAATGCATCCTGATGGAAAGGCATGAGATGGGATTGTTAGAAGACAGAAGGAAAGACAGCCAT
AAATTCTGGCTTGGGAAAACCTCATATCCCCATGAAAGAGAACAAATCACAATAAAAGTGAAGAGTAATGTA
TGGAGCTCTTCACTAGGGTATAAGTAGCTGCAATTGTAATTCTGTTAAAGGAAATCTAGATTATAAC
AACTGCTAGCAAAATGAGGAAACATAAAATTCTCTGAAGAATCATAGGAAGAGTAGACATTATTTATAACC
AATGATATTCTGAGTATATTCTCTCTTTAAAGGAAATCTGATATTGAGTGAATAGGAGAAAACAATATAACACAGA
CTTATTCTCTGTATATTGAGTTTGAGTATATTGAGTGAATAGGAGAAAACAATATAACACACAGA
GAATTAAAGAAAATGACATTCTGGGAGTGGGGATATATATTGTTGAATAACAGAACAGAGTGAAATCTGTTGAATT
AACGGAAAGGGTAAATTAACTCTTGACATCTTCACTCAACCTTCTCATGCTGAGTTAATCTGTTGAATT
GTAGTATTGTTTGTAATTAAACAATAAAAGCCTGCTACATGT



178/249

FIGURE 176

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71883
><subunit 1 of 1, 777 aa, 1 stop
><MW: 89651, pI: 7.97, NX(S/T): 3
MNANKDERLKARSQDFHLFPALMMLSMTMLFLPVTGTLKQNI PRLKLTYKDLLLSNSCIPFL
GSSEGLDFQTLLLDEERGRLLLGAKDHFIFLSSLVDLNKNFKKIYWPAAKERVELCKLAGKDA
NTECANFIRVLQPYNKTHIYVCGTGFHPICGYIDLGVYKEDIIFKLDTHNLESGRLKCPFD
PQQPFASVMTDEYLYSGTASDFLGKDTAFTRSLGPTHDHHYIRTDISEHYWLNGAKFIGTFF
IPDTYNPDDDKIYFFFRESSQEGSTSDKTILSRVGRVCKNDVGGQRSLINKWTTFLKARLIC
SIPGSDGADTYFDELQDIYLLPTRDERNPVVYGVFTTSSIFKGSAVCVYSMADIRAVFNGP
YAHKESADHRWVQYDGRIPYPRPGTCPSKTYDPLIKSTRDFPDDVISFIKRHSVMYKSVYPV
AGGPTFKRINVVDYRLTQIVVDHVIAEDGQYDVMFLGTDIGTVLKVVSIKEKWNMEEVLEEL
LQIFKHSSIILNMELSLKQQQLYIGSRDGLVQLSLHRCDTYGKACADCCLARDPYCAWDGNA
CSRYAPTSKRRARRQDVKYGDPITQCWDIEDSISHEADEKVIFGIEFNSTFLECIPKSQQA
TIKWYIQRSGDEHREELKPDERIIKTEYGLLIRSLQKKDSGMYYCKAQEHTFIHTIVKLTN
VIENEQMENTQRAEHEEGQVKDLLAESRLRYKDYIQILSSPNFSLDQYCEQMWHREKRRQRN
KGGPKWKHMQEMKKKRNRHHRDLDLDELPRAVAT

Important features of the protein:

Signal peptide:

amino acids 1-36

N-glycosylation sites.

amino acids 139-142, 607-610, 724-727

Tyrosine kinase phosphorylation site.

amino acids 571-576

Gram-positive cocci surface proteins 'anchoring' hexapeptide.

amino acids 32-37



179/249

FIGURE 177

CCCTGACCTCCCTGAGCCACACTGAGCTGGAAGCCGAGAGGTATCCTGGAGCATGCCACCGCGGGAGCAGA
CAACCTCCCAGGTAAAGCTGGGAGCAAGACCTGAAGCTGTTCTCAGGAGCCTGGTGTATTTCACCCAC
CTCAGCAGTTCAAGCAGCAGGAGCTGATCAGGTGTGTCTGGAGTGGGAGCAGAAGGCCTGGCTGGCAAGA
GTGGCTGAGGAGAAAGAGGTTCAAGCAGGAGCTGACGGCTTGACCAGCCGAGCTGCCGTGACTACAAGATCCAGAACCATGGCATH
GGGTGAGGAGGGGGCACAGGTGTATGTGCACCTCTTGTCTCAGCAAGAAGAGCTGAGAGAGGGGATCTGG
AGGCACTTGTGAGGAGCTACAGAGGGAGGGAAAGGTATTAAAGTAACAGTGTGGCACAATAGTTAA
GAGCACAGTTTGAGGAGCTAGACCGACATAGGTCATAATTCTCTTGTGAGGAGCTAGTGTGGCACAATAGTTAA
AAGGGAGTGAACCTCTGGACTTCATACTTCTCATCACTAAAGTAGGGCAAAATAGGACCCACCTCAT
AGGGAGATTAAATGACATAATGTATGTGATGCAACTAGCAAAGTACCAAGCTCCATAGTAAGTCATGCCACAG
TATTCCACCCACCCCTGTTCTGCCTTCCAACCAGGTACTGCAACGACTGGAGCAGAGGCGGAGCAGGCTT
CAGAGCGGGAGGCTCCAAGCATAGAACAGAGGTTACAGGAAGTGCAGAGAGCATCCGCCGGCACAGGTGAGCC
AGGTGAAGGGGGCTGCCGGCTGGCCCTGCTGCAGGGGGCTGGCTTAGATGTGGAGCGCTGGCTGAAGCCAGCA
TGACCCAGGCCAGGATGAGGTGGAGCAGGAGCAGGCCGCTCAGTGAGGCTCGGCTGCCAGAGGGACCTCTCTC
CAACCGCTGAGGATGCTGAGCTTCTGACTTGAGGAATGTGAGGAGACGGGAGAGCTTGTGAGGAGCCTGCC
CCAAGCCCTGCCACGAGGCCCTCCCCCTGCCCTGCACACGTGGTATTTCGCTATCAGGCAGGGCGTGAGGATG
AGCTGACAATCACGGAGGGTGAGTGGCTGGAGGTATAGAGGAGGGAGATGCTGACGAATGGGTCAGGCTCGGA
ACACAGCACGGCGAGGTAGGTTGCTGAGCATACTCAACTTCCGACCTCTCCAGAGAGCAGCC
AAGACAGTGACAATCCCTGCGGGCAGAGGCCACAGCATTCTGGCACAGGCCCTGTACAGCTACACCGGACAGA
GTGCAGAGGAGCTGAGCTTCCCTGAGGGGGCACTCATCCGCTGCTGCCCGGGGCCAAGATGGAGTAGATGACG
GCTTCTGGAGGGGGAGAATTGGGGGGCTGTTGGGGCTTCCCCCTCTCTCCAGCTGGTGGAGAGCTGCTGGCCCC
CAGGGCCACCTGAACACTCTGACCCCTGAAACAGATGCTGCCGTCCTCTCTCCAGCTTCTCCCCACCTGAC
CTACCTCTGTTGGATGGGCCCCCTGCACCTGCTCTGGGACAAAGCCCTGGACTTCCCTGGGTTCCCTGG
ACATGATGGCACCTCGACTCAGGCCGATGCGTCCACCACCTCCCCGCCGCTAAAGCCCGGATCCTGGGACC
CAGATCCCCCACCTTGAAGGCCAGGGAGCCTTGACCCCACTGATGCTGCTGCCCTATCTCAAGCTGTCAGA
CCACACCATCAATGATCCAGAGCAACACAGCCAAGCTGGAATGCCCTTATTCACCCCTCACCTCAAGGGT
GGAAACTTGCCCTTCCATTCTAGAGCTGGAACCCACTCCTTTTCCATTGTTCTATCATCTTAGGACC
GGAACACTACCTCTCTGTCATGACCTATCTAGGGTGGTGAATGCCCTGAATCTCTGGGCTGGAAACC
ATCCATCAAGGTCTCTAGTAGTCTGGCCACCTCTTCCCCACCCCTGGCTCCATGACCCACCCACTCTGGATG
CCAGGGTCACTGGGTTGGGCTGGGAGAGGAACAGGCCCTGGGAATCAGGAGCTGGAGGCCAGGATGCGAACAG
CTGTAATGGCTGAGCGGATTATTGACAATGAATAAGGGCACGAAGGCCAGGCCAGGGCTGGCCTTGTG
CTAAGAGGGCAGGGGCCACGGTCTGGGGAGGGCAGGCCAGGGCAGGCCAGCTGCTGCCAC
GCTCTATCATATGGAGCAGGGTCTGGGGAGGGCAGGCCAGGGCAGGCCAGCTGCTGGAGAGCTGGCCAC
TGAGGGGCTGTGACCTCTCTGAGGCCCTGGGAGAGGAACAGGCCCTGGGAATCAGGAGCTGGAGGAGAAGAGAC
ACCTGGGGGGCAGTGTGCTGCCAGTGGAGGGGCTTCAAGGCCACCCCTGGCCCTGGCAGCTGGTAG
TCCATCAGCACAAATGAAGGGAGACTTGGAGAAGAGGAAGATAACACTGTTGCTTCTGTTCAAGCTGTGTCAGC
TTTCCCTGGGCTCCAGGACCTTCCCTACCTCCACCAACCAAGGGATTATAGCAAAGGCTAAGCCTGC
AGTTTACTCTGGGGGTTAGGGAGCCGAAAGGCTAAATAGTTAAGTAGGGTGAATGGGAGAGATGAGATTACCTCA
TTAGGGCTCAGGCAGACTCACCTCACATACTCCCTGCTCCCTGTTGAGAGACACCTGAGAGAAAGGGGAGGG
TCAACAATGAGAGACCAAGGAGTAGGTCTATCAGTGCCCTCAGAGTAGAGAGCAATAAGAGCCCAGCCAGTGC
AGTCCCAGGCTGTGTTCTACCTGGTATCAGAAGTGTCTGGTTGCTGGCTGCCATTGCTCTTGAGTGG
GCAGCCCTGGGCTTGGGCCCTCCCTGCCAGTGTGGCTCTGCAGAAGCTCTGGGTTCCCTCAAGTG
CACGAGGGGTTAGGCTGCTGCCCTGAGTCTCCATCTGTACTGGGGGCTGGCTAGGACCTGGGCTGTGGCC
TCTCAGGGGCCAGCCTCTCCATGGCAGGCACTCCCTGCCCTGGCTGCCCTCCCCAGACCCCTGACCAACCCCTG
GGTCTGTCCTCCCCACAGGCCAGCTCTGCTGCTGGGGAGGGAAACACTGGGTTAGGACCAACTCAGAGGCTGCTG
TCTCAATGTGTGTCACCCGGAAACCTGGGGAGGGAGGGAAACACTGGGTTAGGACCAACTCAGAGGCTGCTG
GCCCTCCCTCTGACCCAGGGACATCCTGAGTTGGCTACTCTCTGCTGGCTAAAGTAGGGGAGGGCTTCTC
AGATTGTGGGGCACATTGTGAGCCTGACTTCTGCTGGAGCTCCAGTCCAGGAGGAAGAGCCAAGGCCACTT
TTGGGATCAGGTGCTGATCACTGGGCCCCCTACCTCAGGCCCTTCTGAGCAGGCCACCTGCCCACTGCCCA
CAGAGAACACAGTGGCTCCCTGTCGGGGGGCGCTTTCTCTCTGAGCAGGCCAGGTGCACTGTTGATGATGGAG
GCCTCTGCTGCGGCTGCAATGGATGCAAGGGGCTGAGAGGCCAGGTGCACTGTTGATGATGGGAGGGGCTC
CGTCCTGCAGGCTGGAGGTGGCATCCACACTGGACAGCAGGAGGGAGGTGAGGGTAACATTCCATTCC
TCATGTTGTTCTACGTTCTCAGCATGCTCTTAAACCCAGAAGGCCAATTCCCAAGGCCATT
TTCTGCTTTATCTAATAACTCAATATTAAG



180/249

FIGURE 178

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73401
><subunit 1 of 1, 370 aa, 1 stop
><MW: 40685, pI: 4.53, NX(S/T): 0
MQLAKYQSHSKCPTVFPPPTVLCLPNQVLQRLEQRQQASEREAPSIEQRLQEVRESIRRA
QVSQVKGAARLALLQAGLDVERWLKPAMTQAQDEVEQERRLSEARLSQRDLSPTAEDAELS
DFEECEETGELFEEPAPQALATRALPCPAHVVFRYQAGREDELTITEGEWLEVIEEGDAEW
VKARNQHGEVGFVPERYLNFPDLSLPESSQDSDNPCGAEPTAFLAQALYSYTGQSAAELSFP
EGALIRLLPRAQDGVDDGFWRGEFGGRGVFPSLLVEELLGPPGPPELSDPEQMLPSPSPPS
FSPPAPTSVLDGPPAPVLPGDKALDFPGFLDMMAPRLRPMRPPPPPAAKAPDPGHPDPLT
```



181/249

FIGURE 179A

CACAGGGAGACCCACAGACACATATGCACGGAGAGACAGAGGAGGAAGAGAGACAGAGACAAAGGCACAGCGGAA
GAAGGCAGAGACAGGGCAGGCACAGAACAGCAGACTCTACAGAGGGAGAGGCCAGAGAACGCTGCAGA
AGACACAGGCAGGGAGAGACAAAGATCCAGGAAGAGGGCTCAGGAGGAGACTTGGAGAACGCCAGACCCCTGG
GCACCTCTCCCAAGCCCCAAGGACTAAGTTTCTCCATTCTTAACGGCTCTCAGGCCCTCTGAAAACCTTGCC
TCTGACCTTGGCAGGGACTCAAGCCCCAAGGCTACAGAGAGGGACTTCCAAGCTAGGGTGTGGAGGACTTGGT
GCCCTAGACGGCCTCAGTCCCCTCCAGCTGAGTACAGTCAGTGCCTCCATTGTGCCGCTCTCTGGCTGGTGTG
CTTGGCAGGGCGCTGGCTGGGGAGCCAACCCCTGCCCTCTGCCAGGGCTGCCAGGCTGTGAGGGACTTGGT
GCTGCTTCTGCTACTGCTGGCTCTCTGCCCTCAGCCCGCTGGCCAGCCCCCTCCCCGGAGGAGGAGAT
CGTGTTCAGAGAAGCTCAACGGCAGCTGCTACTAGAGCTGGAGCAGGACTCCGGTGTGAGGTGAGGGCTGACAGTGCAGTA
GCCCTTGGGGAGACGCTGCTACTAGAGCTGGAGCAGGACTCCGGTGTGAGGTGAGGGCTGACAGTGCAGTA
CCTGGGCCAGGCCTGAGCTGGTGGAGCAGAGCCTGGCACCTACCTGACTGGCACCATCAATGGAGATCC
GGAGTCGGTGGCATCTGCACTGGATGGGGAGCCCTGTTAGGCGTGTACAATATGGGGGCTGAACCTCA
CCTCCAGCCCCCTGGAGGGAGGCACCCCTAACTCTGCTGGGGACCTGGGGCTCACATCTACGCCGAAGAGTCC
TGCCAGCGGTCAAGGTCCCCTGTGCAACGTCAAGGCTCCTCTTGAAGCCCCAGCCCCAGACCCGAAGAGCCAA
GCGCTTGCCTCACTGAGTAGATTGTGGAGACACTGGTGGTGCAGATGACAAGATGGCCGATTCCACGGTGC
GGGGCTAAAGCGTACCTGTAACAGTGATGGCAGCAGCAGCAAGGCCTCAAGCACCCAAGCATTCCGAATCC
TGTCACTGGTGGTCACTGGCTAGTGATCTGGGGTCAAGGGAGGGCCCCAAGTGGGGCCAGTGCTGC
CCAGACCCCTGCGCAGCTCTGTGCTGGCAGCGGGGCTCAACACCCCTGAGGACTCTGGGGCCCTGACCACTTGA
CACAGCATTCTGTTACCCGTCAGGACCTGTGAGGATCTCCACTTGCAACACGCTGGGTATGGCTGATGTGG
CACCGTCTGTGACCCGGCTGGAGCTGTGCCATTGTGGAGGATGATGGCTCCAGTCAGCCTTCACTGCTGCTCA
TGAACGGGTATGCTTCAACATGCTCATGACAACCTCAAGGCATGCACTAGTTGAATGGGCTTGTGAC
CTCTGCCATGTCATGGCCCTGTGATGGCTCATGTGGATCTGAGGAGCCCTGGTCCCCCTGCACTGCCCT
CATCACTGACTTCTGGACAATGGCTATGGCACTGTCCTAGACAAACCAGAGGCTCCATTGCACTGCTGCT
GACTTCCCTGGCAAGGACTATGATGCTGACCGCCAGTGCAGCTGACCTCGGGCCGACTCACGCCATTGTC
ACAGCTGCCGCCGCCGTGCTGCCCTCTGGTGTCTGGCACCTCAATGCCATGCCATGTGCCAGACCAAACA
CTGCCCTGGCGATGGCACACCCCTGCCAGGGCCGCACAGGCCATGGGTGGTCGCTGCCACATGGACCA
GCTCCAGGACTTCAATATTCCACAGGCTGGTGGCTGGGCTCTGGGACCATGGGGACTGCTCTCGGACCTG
TGGGGGTGGTCCAGTTCTCCCTCCGAGACTGCACCGAGGCTGCTCCCCCGGAATGGTGGCAAGTACTGTGAGGG
CCCGCGTACCGCTCCGCTTGCAACACTGAGGACTGCCCAGTGGCTCAGCCCTGACCTTCCGCGAGGAGCA
GTGTGCTGCTCTACAACCCACCGCACCGACCTCTCAAGAGCTTCCAGGGCCATGGACTGGGTCTCGCTACAC
AGGCGTGGGCCCCCGAGGACAGTCAACACTGCCAGGGCCACTGGCTACTACTATGTGCTGGAGCC
ACGGGTGGTAGATGGGACCCCTGTTCCCGAGCAGCTCGTGTGCTCCAGGGCGATCCATGCTGG
CTGTGATGCACTATTGGCTCAAGAAGTAGTTGACAAGTGCACTGGTGTGCGGAGGGAGGGTCTGGTGTGAG
CAAGCAGTCAGGCTCTTCAGGAAATTCAAGGTACGGATAACAATGTGGTCACTATCCCCGGGGGCCACCA
CATTCTGTCCGGCAGGGAAACCCCTGCCACCGGAGCATTCTGGGCTGAAAGCTGCCAGATGGCTCCTA
TGCCCTCAATGGTGAATACACGCTGATGCCCTCCCCACAGATGTGGTACTGCCCTGGGCACTGCCCT
CAGCGGGGCCACTGCAGCCTCAGAGACACTGTCAGGCCATGGGCACTGGCCAGCCTTGACACTGCAAGTCT
AGTGGCTGGCAACCCCCAGGACACACGCCCTCGATACTGCTTCTCGTGCCCGGCCGACCCCTCAACGCCACG
CCCCACTCCCCAGGACTGGCTGACCGAAGAGCACAGATTCTGGAGATCCTCGCGGCCCTGGCGGGCAG
GAAATAACCCTCACTATCCGGCTGCCCTTCTGGGACCGGGGCTCGGACTTAGCTGGGAGAAAGAGAGACT
CTGTTGCTGCCCTCATGCTAAGACTCAGTGGGAGGGCTGTGGCGTGAAGACCTGCCCTCTCTGCCCTAAT
GCCGAGGCTGGCCCTGCCCTGGTTCTGCCCTGGAGGCAGTGATGGGTAGTGGATGGAAGGGCTGACAGAC
AGCCCTCCATCTAAACTGCCCTCTGCCCTGGGGTCACAGGGAGGGAGGGGAAGGCAGGGAGGGCTGGG
CAGTTGATTATTAGTATTTCACCTTATTAGCAGGCCAGGGAAAGGGGACAAGGACTAGGGTCTGGGAA
CCTGACCCCTGACCCCTCATAGCCCTCACCCCTGGGGTAGGAAATCCAGGGTGGTGTGATAGGTATAAGTGGT
TGTGATGCGTGTGTTGAAATGTGTGCTTATGTGAGGTACAACCTGTTCTGCTTCT
TTCCTGAATTATTATTGGAAAAGAAAAGTCAAGGGTAGGGTGGGCTTCAGGGAGTGGGATTATCTTT
TTTTTTTTCTTCTTCTTCTTTTTTTTGAGACAGAATCTCGCTCTGTCGCCAGGCTGGAGTGCATG
GCACAATCTCGGCTCACTGCATCCTCCGCCCTCCGGGTTCAAGTGATTCTCATGCCCTCTGAGTAGCT
GGATTACAGGCTCTGCCACCACGCCAGCTAATTGGTGGGGTTGGAGACAGAGTCTGCTATTGTC
ACCAGGGCTGGAATGATTCACTGCAACCTGCCACCTGGGTTCCAGCAATTCTCCTGCCAGCCTCC
CGAGTAGCTGAGATTAGGCACCTACCAACGCCAGGGCTAATTGGTATTAGTAGAGACGGGTTTCAC
CATGTTGGCCAGGCTGGTCTCGAACTCCTGACCTTAGGTGATCCACTGCCCTCATCTCCAAAGTGTGGATT
ACAGGCGTGAAGCCACCGTGCCTGGCACGCCAACTAATTGGTATTAGTAGAGACAGGGTTACCATGT
TGGCCAGGCTGCTTGAACTCCTGACCTCAGGTAACTGACCTGCCCTCCCAAAGTGTGGGATTACAGG
TGTGAGGCCACCACGCCGGTACATATTAAATTGAATTCTACTATTATGTGATCCTTGGAGTCAGACAG



182/249

FIGURE 179B

ATGTGGTTGCATCCTAACTCCATGTCTTGAGCATTAGATTCTCATTTGCCAATAATAACCTCCCTAGAAG
TTTGTGAGGATTAATAATGTAATAAGAACTAGCATAACACTCAAAAAAAAAAAAAAAAAGGAAA
AAAAAAAAAAAAAAAAAAAAAAAAGGAAA



183/249

FIGURE 180

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73492

><subunit 1 of 1, 837 aa, 1 stop

><MW: 90167, pI: 8.39, NX(S/T): 1

MSQTGSHPGRGLAGRWLWGAQPCLLLPIVPLSWLVWLLLLLASLLPSARLASPLPREEEIV
FPEKLNGSVLPGSGAPARLLCRLQAFGETLLELEQDSGVQVEGLTVQYLGQAPELLGGAEP
GTYLTGTINGDPESVASLHWGGALLGVLQYRGAELHLQPLEGGTPNSAGGPGAHILRRKSP
ASGQGPMCNVKAPLGSPSPRRAKRFASLSRFVETLVVADDKMAAFHGAGLKRYLLTVMAA
AAKAFKHPSIRNPVSLVVTRLVILGSGEEGPVQGPSAAQLRSFCAWQRGLNTPEDSGPDHF
DTAILFTRQDLCGVSTCDTLGMADVGTVCDCPARSCAIVEDDGLQSAFTAHELGHVFNMLHD
NSKPCISLNGPLSTSRRHVMAPVMAHVDPPEPWSPCSARFITDFLDNGYGHCLLDKPEAPLHL
PTVFPGKDYDADRCQLTFGPDSRHCPCQLPPPACAALWCSGHLNGHAMCQTKHSPWADGTPCG
PAQACMGGRCLHMDQLQDFNI PQAGGWGPWGPWGDCSRTCAGGGQFSSRDCTRVPVRNGGKY
CEGRRTFRSCNTEDCPTGSALTFREEQCAAYNHRTDLFKSFPGPMWDVPRYTGVAPQDQCK
LTCQARALGYYYVLEPRVVDGTPCSPDSSVCVQGRCIHAGCDRIIGSKKKFDKCMVCGGDG
SGCSKQSGSFRKFRYGYNNVVTIPAGATHILVRQQGNPGHRSIYLALKLPDGSYALNGEYTL
MPSPTDVVLPGAVSLRYSGATAASETLSGHGPLAQPLTLQVLVAGNPQDTRLRYSFFVPRPT
PSTPRPTPQDWLHRRAQILEILRRRPWAGRK

Important features of the protein:

Signal peptide:

amino acids 1-48

N-glycosylation site.

amino acids 68-71

Glycosaminoglycan attachment site

amino acids 188-191, 772-775

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 182-185

Tyrosine kinase phosphorylation site.

amino acids 730-736

N-myristoylation sites.

amino acids 5-10, 19-24, 121-126, 125-130, 130-135, 147-152, 167-
172, 168-173, 174-179, 323-328, 352-357, 539-544, 555-560, 577-
582, 679-684, 682-687, 763-768

Amidation sites.

amino acids 560-563, 834-837

Leucine zipper pattern.

amino acids 17-38, 24-45

Neutral zinc metallopeptidases, zinc-binding region signature.

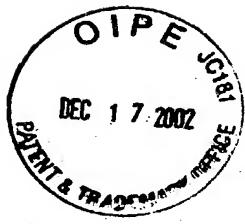
amino acids 358-367



184/249

FIGURE 181

CAGCAGTGGTCTCTCAGCCTCTCAAAGCAAGGAAAGAGTACTGTGTGCTGAGAGACCATGG
CAAAGAACCTCCAGAGAATTGTGAAGACTGTCACATTCTAAATGCAGAAGCTTTAAATCC
AAGAAAATATGTAATCACTTAAGATTGTGGACTGGTGTGTTGGTATCCTGCCCTAACTCT
AATTGTCTGTTGGGGAGCAAGCACTTCTGCCGGAGGTACCCAAAAAGCCTATGACA
TGGAGCACACTTCTACAGCAATGGAGAGAAGAAGAAGATTACATGAAATTGATCCTGTG
ACCAGAACTGAAATATTCAAGCGAAATGGCACTGATGAAACATTGAAAGTGCACGACTT
TAAAAACGGATACTGGCATCTACTCGTGGTCTCAAAATGTTATCAAAACTCAGA
TTAAAGTGATTCTGAATTCTGAACCAGAAGAGGAAATAGATGAGAATGAAAGAAATTACC
ACAACCTTCTTGAAACAGTCAGTGATTGGTCCCAGCAGAAAAGCCTATTGAAAACCGAGA
TTTCTTAAATTCCAAAATTCTGGAGATTGTGATAACGTGACCATGTATTGGATCAATC
CCACTCTAATATCAGTTCTGAGTTACAAGACTTGAGGAGGGAGAAGATCTTCACTTT
CCTGCCAACGAAAAAAAGGGATTGAACAAAATGAACAGTGGTGGTCCCTCAAGTGAAGT
AGAGAAGACCGTCACGCCAGACAAGCAAGTGGAGAAGAACCTCCAATAATGACTATACTG
AAAATGGAATAGAATTGATCCCATGCTGGATGAGAGAGGTTATTGTTGTATTACTGCCGT
CGAGGCAACCGCTATTGCCCGCGTCTGTGAACCTTACTAGGCTACTACCCATATCCATA
CTGCTACCAAGGAGGACGAGTCATCTGTCGTCTCATGCCCTGTAAGTGGTGGTGGCC
GCATGCTGGGAGGGTCTAATAGGAGGTTGAGCTCAAATGCTAAACTGCTGGCAACATAT
AATAATGCATGCTATTCAATGAATTCTGCCTATGAGGCATCTGGCCCTGGTAGCCAGCT
CTCCAGAATTACTGTAGGTAATTCTCTCTCATGTTCTAAACTTCTACATTATCACC
AAAAAAAAAAAAAA



185/249

FIGURE 182

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73727
><subunit 1 of 1, 317 aa, 1 stop
><MW: 37130, pI: 5.18, NX(S/T): 3
MAKNPPENCEDCHILNAEAFSKKICKSLKICGLVFGILALTLIVLFWGSKHFPEVPKKAY
DMEHTFYNSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKT
QIKVIPEFSEPEEEIDENEETTTFEQSVIWVPAEKPIENRDFLKNSKILEICDNVTMYWI
NPTLISVSELQDFEEEDEDLHFPAKEKKGIEQNEQWVVPQVKVEKTRHARQASEEEELPINDY
TENGIEFDPMLERGYCCIYCRRGNRYCRRVCEPLLGYYPYCYQGGRVICRVIMPCNWV
ARMLGRV
```

Important features of the protein:

Signal peptide:

amino acids 1-40

Transmembrane domain:

amino acids 25-47 (type II)

N-glycosylation sites.

amino acids 94-97, 180-183

Glycosaminoglycan attachment sites.

amino acids 92-95, 70-73, 85-88, 133-136, 148-151, 192-195, 239-242

N-myristoylation sites.

amino acids 33-38, 95-100, 116-121, 215-220, 272-277

Microbodies C-terminal targeting signal.

amino acids 315-317

Cytochrome c family heme-binding site signature.

amino acids 9-14



186/249

FIGURE 183

GCAGGAACCTGGCTCCGGCTGGCACCTGAGGAGCGGCCGTGACCCCGAGGGCCCAGGGAGCTGCC
CGGCTGGCCTAGGCAGGCAGCCGCACCATGGCCAGCACGGCCGTGCAGCTCTGGGCTTCCT
GCTCAGCTTCCTGGCATGGTGGCACGTTGATCACCAACATCCTGCCGCACTGGCGGAGGA
CAGCGCACGTGGCACCAACATCCTCACGGCGTGTCCCTACCTGAAAGGGCTCTGGATGGAG
TGTGTGTGGCACAGCACAGGCATCTACCAAGTGCAGATCTACCGATCCCTGCTGGCGCTGCC
CCAAGACCTCCAGGCTGCCCGCCCTCATGGTCATCTCCTGCCCTCGGCGATAGCCT
GCGCCTGCCCGTCATCGGGATGAAGTGACCGCCTGCACGGCACACCCGCCAACGACC
ACCTTGCCATCCTCGCGGCACCCCTTCATCCTGCCGGCCTCCTGTGCATGGTGGCGT
CTCCTGGACCACCAACGACGTGGTGCAGAACTTCTACAACCCGCTGCTGCCAGCGGCATGA
AGTTTGAGATTGGCCAGGCCCTGTACCTGGGCTTCATCTCCTCGTCCCTCTCGCTATTGGT
GGCACCCCTGCTTGCCCTGCCAGGACGGAGGCACCCCTACAGGCCCTACCGAGGCCCGCC
CAGGGCCACCACGACCACTGCAAACACCGCACCTGCCCTACAGGCCACAGCTGCCCTACAAAG
ACAATCGGGCCCCCTCAGTGACCTCGGCCACGCACAGCGGTACAGGCTGAACGACTACGTG
TGAGTCCCCACAGCCTGCTCTCCCTGGGCTGCTGTGGCTGGGTCCCCGGGGACTGTC
AATGGAGGCAGGGGTTCCAGCACAAAGTTACTTCTGGCAATTTGTATCCAAGGAAATA
ATGTGAATGCGAGGAAATGTCTTAGAGCACAGGGACAGAGGGGAAATAAGAGGAGGAGAA
AGCTCTCTACCAAAAGACTGAAAAAAAATCCTGTCTGTTTGATTTATTATATATAT
TTATGTGGGTGATTGATAACAAGTTAATATAAAAGTGAATTGGAGTTGGTCAGTGGGT
TGGTTGTGATCCAGGAATAAACCTGCGGATGTGGCTGTTATGAAAAAAA



187/249

FIGURE 184

MASTAVQLLGFLLSFLGMVGTLITLPHWRRTAHVGTNILTAVSYLKGLWMECVWHSTGIY
QCQIYRSLLALPQDLQAARALMVISCLLSGIACACAVIGMKCTRCAKTPAKTTFAILGGTL
FILAGLLCMVAWSWTNDVVQNFYNPPLPSGMKFEIGQALYLGFISSSLSLIGGTLCLSCQ
DEAPYRPYQAPPRATTTTANTAPAYQPPAAYKDNRAPSVTSAATHSGYRLNDYV

Important features of the protein:

Signal peptide:

amino acids 1-21

Transmembrane domains:

amino acids 82-103, 115-141, 160-182



188/249

FIGURE 185

GAGCTCCCTCAGGAGCGCGTTAGCTTCACACCTCGGCAGCAGGAGGGCGGCAGCTTCTCG
CAGGCAGGGCGGGCGGCCAGGATC**ATG**TCCACCACATGCCAAGTGGTGGCGTTCCCT
CCTGTCCATCCTGGGCTGGCCGGCTGCATCGCGGCCACCAGGATGGACATGTGGAGCACCC
AGGACCTGTACGACAACCCCGTCACCTCCGTGTTCCAGTACGAAGGGCTCTGGAGGAGCTGC
GTGAGGCAGAGTTCAGGCTTCACCGAATGCAGGCCCTATTCACCATCCTGGGACTTCCAGC
CATGCTGCAGGCAGTGCAGGCCCTGATGATCGTAGGCATCGCCTGGGTGCCATTGGCCTCC
TGGTATCCATTTGCCCTGAAATGCATCCGCATTGGCAGCATGGAGGACTCTGCCAAAGCC
AACATGACACTGACCTCCGGGATCATGTTCAATTGTCTCAGGTCTTGCAATTGCTGGAGT
GTCTGTGTTGCCAACATGCTGGTACTAACCTCTGGATGTCCACAGCTAACATGTACACCG
GCATGGGTGGGATGGTCAGACTGTTCAGACCAGGTACACATTGGTGGCTCTGTTCTG
GGCTGGGTCGCTGGAGGCCTCACACTAATTGGGGGTGTGATGATGTGCATGCCCTGCCGGGG
CCTGGCACCAGAAGAAACCAACTACAAAGCCGTTCTATCATGCCCTCAGGCCACAGTGTG
CCTACAAGCCTGGAGGCTCAAGGCCAGCACTGGCTTGGTCCAACACCAAAAACAAGAAG
ATATAACGATGGAGGTGCCCGCACAGAGGACGAGGTACAATCTATCCTCCAAGCACGACTA
TGTG**TAAT**GCTCTAACGACCTCTCAGCACGGCGGAAGAAACTCCGGAGAGCTACCCAAAA
AACAAAGGAGATCCCCTAGATTCTTCTGTTGACTCACAGCTGGAAAGTTAGAAAAGC
CTCGATTCATCTTGGAGAGGCCAAATGGCTTAGCCTCAGTCTGTCTCTAAATATTCC
ACCATAAAACAGCTGAGTTATTATGAATTAGAGGCTATAGCTCACATTTCATCCTCTAT
TTCTTTTTAAATATAACTTCTACTCTGATGAGAGAATGTGGTTAATCTCTCTCAC
ATTTGATGATTTAGACAGACTCCCCCTTCCCTCAGTCAATAACCCATTGATGATCTA
TTTCCCAGCTATCCCCAAGAAAACCTTGAAAGGAAAGAGTAGACCCAAAGATGTTTT
CTGCTGTTGAATTTGTCTCCCCACCCCAACTGGCTAGTAATAAACACTTACTGAAGAA
GAAGCAATAAGAGAAAGATATTGTAATCTCTCCAGCCATGATCTGGTTTCTACACTG
TGATCTAAAAGTTACCAAACCAAGTCATTTCAGTTGAGGCAACCAAACCTTCTACTG
CTGTTGACATCTCTTATTACAGCAACACCATTCTAGGAGTTCTGAGCTCTCCACTGGAG
TCCTCTTCTGTCGGGGTCAGAAATTGCTTAGATGAATGAGAAAATTATTTTTAAT
TTAAGTCCTAAATATAGTTAAAATAAATAATGTTAGTAAAATGATACACTATCTCTGTGA
AATAGCCTCACCCCTACATGTGGATAGAAGGAAATGAAAAATAATTGCTTGACATTGTCT
ATATGGTACTTGTAAAGTCATGCTTAAGTACAAATTCCATGAAAAGCTCACACCTGTAATC
CTAGCACTTGGGAGGCTGAGGAGGAAGGATCACTTGAGCCAGAAGTTCGAGACTAGCCTG
GGCAACATGGAGAAGCCCTGTCTCACAAATAACAGAGAGAAAAATCAGCCAGTCATGGTG
GCATACACCTGTAGTCCCAGCATTCCGGGAGGCTGAGGTGGGAGGATCACTTGAGCCCAGGG
AGGTTGGGCTGCAGTGAGCCATGATCACACCACTGCACTCCAGCCAGGTGACATAGCGAGA
TCCTGTCTAAAAAATAAATAATGGAACACAGCAAGTCCTAGGAAGTAGGTTAAA
ACTAATTCTTAA



189/249

FIGURE 186

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73734
><subunit 1 of 1, 261 aa, 1 stop
><MW: 27856, pI: 8.50, NX(S/T): 1
MSTTCQVVAFLLSILGLAGCIAATGMDMWSTQDLYDNPVTSVFQYEGLWRSCVRQSSGFTE
CRPYFTILGLPAMLQAVRALMIVGIVLGAIGLLVSI FALKCIRIGSMEDSAKANMTLTSGIM
FIVSGLCAIAGVSVFANMLVTNFWMSTANMYTGMGGMVQTVQTRYTFGAALFVGWVAGGLTL
IGGVMMCIACRGLAPEETNYKAVSYHASGHHSVAYKPGGFCASTGFGSNTKNKKIYDGGARTE
DEVQSYP SKHDYV
```

Signal peptide:

amino acids 1-23

Transmembrane domains:

amino acids 81-100, 121-141, 173-194

**FIGURE 187**

GGAAAAACTGTTCTTCTGTGGCACAGAGAACCTGCTCAAAGCAGAAGTAGCAGTTCCG
GAGTCCAGCTGGCTAAAACATCCCAGAGGATA**ATG**GCAACCCATGCCTAGAAATCGCTG
GGCTGTTCTGGTGGTGGAAATGGTGGGCACAGTGGCTGTCAGTGTATGCCCTAGTGG
AGAGTGTGGCCTTCATTGAAAACAACATCGTGGTTTGAAAACCTCTGGGAAGGACTGTG
GATGAATTGCGTGAGGCAGGCTAACATCAGGATGCAGTGCAAAATCTATGATTCCCTGCTGG
CTCTTCTCCGGACCTACAGGCAGGCCAGAGGACTGATGTGCTGCTCCGTATGTCCTTC
TTGGCTTCATGATGGCCATCCTGGCATGAAATGCACCAGGTGCACGGGGACAATGAGAA
GGTGAAGGCTCACATTCTGCTGACGGCTGGAATCATCTCATCACGGCATGGTGGTGC
TCATCCCTGTGAGCTGGTTGCCAATGCCATCATCAGAGATTCTATAACTCAATAGTGAAT
GTTGCCAAAAACGTGAGCTGGAGAAGCTCTACTTAGGATGGACCACGGCACTGGTGCT
GATTGTTGGAGGAGCTCTGTTCTGCTGCGTTTGCAACGAAAAGAGCAGTAGCTACA
GATACTCGATACTTCCCATCGCACAAACCAAAAAAGTTATCACACCGGAAAGAAGTCACCG
AGCGTCTACTCCAGAAGTCAGTATGTG**TAG**TTGTGTATGTTTTAACTTTACTATAAGC
CATGCAAATGACAAAATCTATATTACTTTCTAAAATGGACCCAAAGAAACTTGATTAA
CTGTTCTTAACTGCCAATCTTAATTACAGGAACGTGCATCAGCTATTGATTCTATAA
GCTATTCAGCAGAATGAGATATTAAACCAATGCTTGTATTGTTCTAGAAAGTATAGTAAT
TTGTTCTAAGGTGGTTCAAGCATTACTCTTTATCATTACTTCAAAATGACATTGCT
AAAGACTGCATTATTTACTACTGTAATTCTCCACGACATAGCATTATGTACATAGATGAG
TGTAACATTATCTCACATAGAGACATGCTTATGGTTATTAAAATGAAATGCCAG
TCCATTACACTGAATAAATAGAACTCAACTATTGCTTTCAGGGAAATCATGGATAGGGTG
AAGAAGGTTACTATTAAATTGTTAAAACAGCTAGGGATTAATGTCCTCCATTATAATGA
AGATTAAAATGAAGGCTTAATCAGCATTGTAAGGAAATTGAATGGCTTCTGATATGCTG
TTTTTAGCCTAGGAGTTAGAAATCCTAACCTCTTATCCTCTCCAGAGGCTTTT
TTCTGTGTATTAAATTAAACATTAAAACGCAGATATTGTCAGGGCTTTGCATTCA
AACTGCTTCCAGGGCTACTCAGAAGAAAGATAAAAGTGTGATCTAAGAAAAGTGTG
GTTTAGGAAAGTGAAAATATTGTTGTATTGAAGAAGAATGATGCATTGACAA
GAAATCATATGTATGGATATTAAATAAGTATTGAGTACAGACTTGAGGTTCATC
AATATAAAATAAGAGCAGAAAAATATGCTTGGTTTCATTGCTTACCAAAAAACAACA
ACAAAAAAAGTTGCTTGGAGAACCTCACCTGCTCCTATGTGGGTACCTGAGTCAGGAA
TCATTGTTCTGTGAAAATAAAATTCTTCTGTACCTTCTGTTAGTTACTAAA
ATCTGTAAATACTGTATTCTGTTATTCCAATTTGATGAAACTGACAATCCAATTGA
AAGTTGTGTCGACGTCTGTCTAGCTAAATGAATGTGTTCTATTGCTTATACATTATA
TTAATAAAATTGTACATTCTAATT



191/249

FIGURE 188

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73735
><subunit 1 of 1, 225 aa, 1 stop
><MW: 24845, pI: 9.07, NX(S/T): 0
MATHALEIAGLFLGGVGMVGTAVTVMPQWRVSIFIENNIVVFENFWEGLWMNCVRQANIRM
QCKIYDSILLALSPDLQAARGLMCAASVMSFLAFMAILGMKCTRCTGDNEKVKAHILLTAGI
IFIITGMVVLIPVSWANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIVGGALFCCVF
CCNEKSSSYRYSIPSHRTTQKSYHTGKKSPSVYSRSQYV

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 82-101, 118-145, 164-188



192/249

FIGURE 189

TCGCCATGGCCTCTGCCCGGAATGCAGATCCTGGGAGTCGTCCGTACACTGCTGGGCTGGGTG
AATGGCCTGGTCTCCTGTGCCCTGCCCATGTGGAAGGTGACCGCTTCATCGGCAACAGCAT
CGTGGTGGCCCAGGTGGTGTGGAGGGCCTGTGGATGTCCCTGCGTGGTGCAGAGCACCGGCC
AGATGCAGTGCAAGGTGTACGACTCACTGCTGGCGCTGCCACAGGACCTGCAGGGCTGCACGT
GCCCTCTGTGTACGCCCTCCTGTGGCCCTGTTGGCTGCTGGTCTACCTTGCTGGGC
CAAGTGTACCACCTGTGTGGAGGAGAAGGATTCCAAGGCCCGCCTGGTGCACCTCTGGGA
TTGTCTTGTACATCTCAGGGGTCCGTACGCTAATCCCCGTGTGCTGGACGGCGATGCCATC
ATCCGGGACTTCTATAACCCCCTGGTGGCTGAGGCCAAAGCAGGGAGCTGGGGCCTCCCT
CTACTTGGGCTGGCGGCCCTCAGGCCTTTGTTGCTGGGTGGGGTTGCTGTGCTGCACTT
GCCCTCGGGGGGGTCCCAGGCCCAAGGCCATTACATGGCCCGCTACTCAACATCTGCCCT
GCCATCTCTGGGGGCCCTTGAGTACCCCTACCAAGAATTACGTCTGACGTGGAGGGAAATG
GGGGCTCCGCTGGCGTAGAGCCATCCAGAAGTGGCAGTGCCCAACAGCTTGGATGGGTT
CGTACCTTTGTTCTGCCTCCTGCTATTTTCTTGACTGAGGATATTAAAATTCAATT
AAAAACTGAGCCAAGGTGTTGACTCAGACTCTCACTTAGGCTCTGCTGTTCTCACCTGG
ATGATGGAGCAAAGAGGGATGCTTGAGATTCTGGATCTGACATGCCATCTAGAAC
CAGTCAAGCTATGGAACTAATGCGGAGGCTGCTGCTGTGCTGGCTTGCAACAAGACAGAC
TGTCCCCAAGAGTCCTGCTGCTGGGGCTGGCTCCCTAGATGTCAGTGACAGCTG
CCCCCCTACTCAGGTCTCTGGAGCTCCTCTTCACCCCTGGAAAAACAAATCATCTG
TTAACAAAGGACTGCCACCTCCGGAACCTCTGACCTCTGTTCTCCGTCTGATAAGACG
TCCACCCCCCAGGGCCAGGTCCCAGCTATGTAGACCCCCGCCCCACCTCCAACACTGCACC
CTTCTGCCCTGCCCTCGTCTCACCCCTTACACTCACATTATCAAATAAAGCATG
TTTGTTAGTGCA



193/249

FIGURE 190

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73736
><subunit 1 of 1, 220 aa, 1 stop
><MW: 23292, pI: 8.43, NX(S/T): 0
MASAGMQILGVVLTLLGWVNGLVSCALPMWKVTAFIGNSIVVAQVVWEGLWMSCVVQSTGQM
QCKVYDSLLALPQDLQAARALCVIALLVALFGLLVYLAGAKCTTCVEEKDSKARLVLTS
FVISGVLTLPVCWTAHAIIRDFYNPLVAEAQKRELGASLYLGWAASGLLLLGGGLLCCTCP
SGGSQGPSPHYMARYSTSAPAISRGPSEYPTKNYV
```

Transmembrane domains:

amino acids 8-30 (type II), 82-102, 121-140, 166-186



194/249

FIGURE 191

GCCAAGGAGAACATCATCAAAGACTTCTAGACTCAAAAGGCTTCACGTTACATCTTG
AGCATCTTCTACCACTCCGAATTGAACCAGTCTCAAAGTAAAGGCAATGGCATTATCCC
TTGCAAATTGCTGGCTGGTTCTGGGTCTGGCATGGTGGGGACTCTGCCACAACCCT
TCTGCCTCAGTGGTGGAGTATCAGCTTGTGGCAGCAACATTATTGTCTTGAGAGGCTC
TGGGAAGGGCTTGG**A**TTGCATCCGACAAGCCAGGGTCCGGTTGCAATGCAAGTTCTA
TAGCTCCTTGTGGCTCTCCGCCTGCCCTGGAAACAGCCCAGGCCCCCTCATGTGTGGCTG
TTGCTCTCCTTGATGCCCTGCTTATTGGCATCTGTGGCATGAAGCAGGTCCAGTGCACA
GGCTCTAACGAGAGGGCAAAGCATACCTCTGGAACTTCAGGAGTCCTCATCCTGAC
GGGTATCTCGTTCTGATTCCGGTGAGCTGGACAGCCAATATAATCATCAGAGATTTCTACA
ACCCAGCCATCCACATAGGTCAAGAACGAGAGCTGGGAGCAGCACTTTCTGGCTGGCA
AGCGCTGCTGTCCTCTTCATTGGAGGGGTCTGCTTGTGGATTGCTGCTGCAACAGAAA
GAAGCAAGGGTACAGATATCCAGTGCCTGGCTACCGTGTGCCACACACAGATAAGCGAAGAA
ATACGACAATGCTTAGTAAGACCTCCACCAGTTATGTCTAATGCCTCTTGGCTCCAAGT
ATGGACTATGGTCAATGTTTTATAAAGTCCTGCTAGAAACTGTAAGTATGTGAGGCAGGA
GAACCTGCTTATGTCTAGATTACATTGATACGAAAGTTCAATTGTTACTGGTGGTAGG
AATGAAAATGACTTACTGGACATTCTGACTTCAGGTGTATTAAATGCATTGACTATTGTTG
GACCCAATCGCTGCTCCAATTTCATATTCTAAATTCAAGTATAACCCATAATCATTAGCAAG
TGTACAATGATGGACTACTTATTACTTTGACCATCATGTATTATCTGATAAGAATCTAAA
GTTGAAATTGATATTCTATAACAATAAAACATATACCTATTCTA



195/249

FIGURE 192

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73737  
><subunit 1 of 1, 173 aa, 1 stop  
><MW: 18938, pI: 9.99, NX(S/T): 1  
MNCIRQARVRLQCKFYSSLLALPPALETARALMCVAVALSLIALLIGICGMKQVQCTGSNER  
AKAYLLGTSGVLFILTGIFVLIPVSWTANIIIRDIFYNPAIHIGQKRELGAALFLGWASAAVL  
FIGGGLLCGFCCCNRKKQGYRYPVPGYRVPHTDKRRNTTMLSKTSTSYV
```

Important features of the protein:

Transmembrane domains:

amino acids 31-51, 71-90, 112-133

N-glycosylation site.

amino acids 161-164



196/249

FIGURE 193

AGTGACAATCTCAGAGCAGCTTCTACACCACAGCCATTCCAGC**ATGAAGATCACTGGGGT**
CTCCTTCTGCTCTGTACAGTGGTCTATTCTGTAGCAGCTCAGAAGCTGCTAGTCTGTCTCC
AAAAAAAGTGGACTGCAGCATTACAAGAAGTATCCAGTGGTGGCCATCCCCCTGCCCATCA
CATACCTACCACTTGTGGTTCTGACTACATCACCTATGGGAATGAATGTCACTTGTGTACC
GAGAGCTTGAAAAGTAATGGAAGAGTTCAGTTCTTCACGATGGAAGTTGC**TAA**ATTCTCCA
TGGACATAGAGAGAAAGGAATGATATTCTCATCATCATCTTCATCATCCCAGGCTCTGACTG
AGTTTCTTCAGTTTACTGATGTTCTGGGTGGGGACAGAGCCAGATTCAAGAGTAATCTTG
ACTGAATGGAGAAAGTTCTGTGCTACCCCTACAAACCCATGCCTCACTGACAGACCAGCAT
TTTTTTTTAACACGTCAATAAAAAAATAATCTCCCAGA



197/249

FIGURE 194

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73739

><subunit 1 of 1, 85 aa, 1 stop

><MW: 9232, pi: 7.94, NX(S/T): 0

MKITGGLLLLCTVYYFCSSSEAASLSPKKVDCSIYKKYPVVAIPCPITYLPVCGSDYITYGN
ECHLCTESLKSNGRVQFLHDGSC

Signal peptide:

amino acids 1-19



198/249

FIGURE 195

CCCGCGCCCGGTTCTCCCTCGCAGCACCTCGAACGTGCGCCCTGCCCTCCTGCTCGCGCCC
CGCCGCCATGGGCTGCCTCCCCCGCGCGGCCCTGCTGTCCTGGCCCTGACCGGGCTGGCGCTGC
TCCTGCTCCTGTGCTGGGCCAGGTGGCATAAAGTGGAAATAAACTCAAGCTGATGCTCAA
AAACGAGAAGCACCTGTTCCA ACTAAGACTAAAGTGGCCGTTGATGAGAATAAGCCAAAGA
ATTCCCTTGGCAGCCTGAAGCGCCAGAACGCGCAGCTGTGGACCGGACTCGGCCCGAGGTGC
AGCAGTGGTACCAGCAGTTCTACATGGGCTTGATGAAGCGAAATTGAAGATGACATC
ACCTATTGGCTTAACAGAGATCGAAATGGACATGAATACTATGGCGATTACTACCAACGTCA
CTATGATGAAGACTCTGCAATTGGTCCCCGGAGCCCTACGGCTTAGGCATGGAGCCAGCG
TCAACTACGATGACTACTAACCATGACTGCCACACGCTGTACAAGAAGCAAATAGCGATTC
TCTTCATGTATCTCCTAACACTACTTGGTTCTGATTTGCTCTATTCAGCAGAT
CTTTTCTACCTACTTGTGATCAAAAAAGAAGAGTTAAAACAACACATGTAATGCCTTT
TGATATTCATGGGAATGCCTCTCATTTAAAAATAGAAATAAGCATTGTTAAAAAGA



199/249

FIGURE 196

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73742

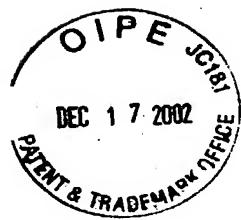
><subunit 1 of 1, 148 aa, 1 stop

><MW: 17183, pI: 8.77, NX(S/T): 0

MAASPARPAVLALTGLALLLLCWGP GG ISGNKLKMLQKREAPVPTKTKAVDENKAKEFL
GSLKRQKRQLWDRTRPEVQQWYQQFLYMGFDEAKFEDDITYWLNRDRNGHEY YGDYYQRHYD
EDSAIGPRSPYGFRHGASVNYDDY

Signal peptide:

amino acids 1-30



200/249

FIGURE 197

CGGCTCGAGCCGCCGGAAAGTGCCGAGGGGCCGATGGAGCTGGGGAGCCGGCGCTC
GGTAGCGCGGGCAAGGCAGGCAGGCCATGACCTGATTGAAGGGTGGGTGATGAGGTGAC
CGTCCTTTCTCGGTGCTTGCCCTGCCCTCTGGTGCTGCCCTGCCCTGGTCTAACGCACA
CCGCTGAGGGCGGGGACCCACTGCCCGTCAGGGACCCAACGCCATCCCAGCCCAGC
GCAGCCATGGCAGCTACCGACAGCATGAGAGGGAGGCCAGGGCAGAGACCCCCAGCCT
GAGACACAGAGGTCAAGCTGCACAGCCAGAGCCCAGCACGGGTTCACAGCAACACCAGCAG
CCCCGGACTCCCCGAGGAGCCCTCGTGCACGGCTGAAATTCCCTCAATGATTAGCAG
GTGGCCAGGGCTGGCCCCACGACACCATTGGCTCCTGAAAAGGACCCAGTTCCGGCCG
GGAACAGCAGGTGCGACTCATCTACCAAGGGCAGCTGCTAGGCGACGACACCCAGACCCCTGG
GCAGCCTCACCTCCCTCCAACTGCCTCTCCACTGCCACGTGTCACGAGAGTCGGTCCC
CCAAATCCCCCTGCCGCCGGGTCCGAGCCCGGCCCTCCGGGCTGGAAATCGGCAGCCT
GCTGCTCCCCCTGCTGCTCCTGCTGTTGCTGCTGCTCTGGTACTGCCAGATCCAGTACCGC
CCTTCTTCCCCCTGACGCCACTCTGGCCTGGCCGGCTTCACCTGCTCCTCAGTCTCCTG
GCCTTGCCATGTACCGCCCGTAGGCCTCCGCGGGCCTGGCAGCGTCGCCGGCCCTCC
GGACCTTGCTCCCCGCCGCCGGAGCTGCTGCCAGGCCCTCTCCGGCCTG
CCTCTCCGCTGCCCTGGAGGCCAGCCCTGCCCGCAGAGGACTCCGGACTGGCGGAGG
CCCCGCCCTGCGACCGCCGGGCTCGGGCACCTCCGGGCTGCTGAACCTCAGCCCGCA
CTGGGAGTGGCTCCTCGGGCTGGGATCTGCTGCTGCCCTGCCCTGGGAGAGCCG
GGCCGCCCGGGGGCCGCTTAGTGGCTGCCGGAGGACCCAGCCGCCCTCCAATCCCTGAC
AGCTCCTGGCTGAGTTGGGACGCCAGGTGGTGGAGGCTGGTAAGGGAGCGGGAG
GGCAGAGGAGTTCCCCGAAACCGTGCAGATTAAAGTAAGTGAAGTTAAAAAAAAAA
AAAAAAA



201/249

FIGURE 198

MTLIEVGVDVTVLFSVLACLLVLALAWVSTHTAEGGDPLPQPSGTPTPSQPSAAMAATDSM
RGEAPGAETPSLRHRGQAAQPEPSTGFTATPPAPDSPQEPLVRLKFLNDSEQVARAWPHDT
IGSLKRTQFPGREQQVRLIYQGQLLGDDTQTLGSLHLPPNCVLHCHVSTRVGPPNPPCPPGS
EPGPSGLEIGSLLLPLLLLLLWYCQIQYRPFFPLTATLGLAGFTLLSLLAFAMYRP

Signal peptide:

amino acids 1-31

Transmembrane domain:

amino acids 195-217



1000 1001 1002 1003 1004 1005 1006 1007 1008 1009

202/249

FIGURE 199

GAGATTGGAAACAGCCAGGTTGGAGCAGTGAGTGAGTAAGGAAACCTGGCTGCCCTCTCCAG
ATTCCCCAGGCTCTCAGAGAAGATCAGCAGAAAGTCTGCAAGACCCTAACGAACCATCAGCCC
TCAGCTGCACCTCCTCCCTCCAAGGATGACAAAGGCGCTACTCATCTATTGGTCAGCAGC
TTCTGCCCTAAATCAGGCCAGCCTCATCAGTCGCTGTGACTTGGCCCAGGTGCTGCAGCT
GGAGGACTTGGATGGGTTGAGGGTTACTCCCTGAGTGACTGGCTGTGCCTGGCTTTGTGG
AAAGCAAGTTAACATATCAAAGATAAATGAAAATGCGGATGGAAGCTTGACTATGCCCTC
TTCCAGATCAACAGCCACTACTGGTGCAACGATTATAAGAGTTACTCGGAAACCTTGCA
CGTAGACTGTCAAGATCTGCTGAATCCAACCTTGCAGGCATCCACTGCGAAAAAGGA
TTGTGTCCGGAGCACGGGGATGAACAACGGTAGAATGGAGGTTGCAGTGTCAAGGCCGG
CCACTCTCCTACTGGCTGACAGGATGCCGCTGAGATGAAACAGGGTGCAGGTGCACCGTGG
AGTCATTCCAAGACTCCTGTCCTCACTCAGGGATTCTTCATTCTTCTTCCACTGCCTCCA
CTTCATGTTATTTCTTCCCTCCATTACAACAAAAGCTGACCAGAGCCCCAGGAATAAA
TGGTTTCTTGGCTTCCTCCTTACTCCCATCTGGACCCAGTCCCTGGTTCTGTGTAT
TTGTAAACTGAGGACCACAATAAGAAATCTTATATTATCG

FIGURE 200

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73746
><subunit 1 of 1, 148 aa, 1 stop
><MW: 16896, pI: 6.05, NX(S/T): 1
MTKALLIYLVSSFLALNQASLISRCDLAQVLQLEDLDGFEGYSLSDWLCLAFVESKFNISKI
NENADGSFDYGLFQINSHYWCNDYKSYSENLCHVDCQDLLNPNLLAGIHCAKRVSGARGMN
NWVEWRLHCSGRPLSYWLTGCRLR
```

Signal peptide:

amino acids 1-18



204/249

FIGURE 201

TCTGACCTGACTGGAAGCGTCCAAAGAGGGACGGCTGTCAGCCCTGCTTGACTGAGAACCCA
CCAGCTCATCCCAGACACCTCATAGCAACCTATTATACAAAGGGGAAAGAACACCTGAG
CAGAATGGAATCATTATTTTTCCAAGGAGAAAACCGGGTAAAGGGAGGGAAAGCAATT
AATTGAGTCCTGTGAATGGGCTTCAAGGCAATTAAAGAAATCCACTCAGAGAGGAC
TTGGGGTCAAACCTGGGCTCTGTGGTTCTGATTGTAAGTGGAAAGCAGGTCTGCACACGC
TGTTGGCAAATGTCAGGACCAGGTTAAGTGAAGCAGAAAAACTCAGGTGGAACAAGCA
ACCCATGTTCTGCAAGCTTGAAAGGAGCCTGGAGCGGGAGAAAGCTAACTTGAACATGAC
CTGTTGCATTGGCAAGTTCTAGCAACATGCTCCTAACAGGAAAGCATAAGGCACAGACCATG
CAGACTCCAGTCCCTGCTGCTCTGATGCTGGGATGCGTCCTGATGATGGTGGCGATGT
TGCACCCCTCCCCACCACACCCCTGCAACAGACTGTCACAGCCCAAGCCAGCAAGCACAGCC
GAAGCCAGGTACCGCCTGGACTTGGGAATCCCAGGATTGGGTACTGGAAGCTGAGGATGA
GGGTGAAGAGTACAGCCCTCTGGAGGGCCTGCCACCCCTTATCTCACTGCGGGAGGATCAGC
TGCTGGTGGCGTGGCTTACCCCAGGCCAGAAGGAACCAAGAGCCAGGGCAGGAGAGGTGG
AGCTACCCGCTCATCAAGCAGCAAGGAGGAGGATAAGGAAGCCCCAAAGAGGGACTGGG
GGCTGATGAGGACGGGGAGGTGTCGAAGAAGAGGAGTTGACCCGTTCAGCCTGGACCCAC
GTGGCCTCCAGGAGGCACTCAGTCCCCGATCCCCCTCCAGAGGGCTTGCCCGAGGTGCGG
CACCCACTGTGTCAGCAGCACCTCAGGACAGCCTGCCACAGCCAGCGTACCTCTG
TTTCCATGATGAGGCCTGGTCCACTCTCCTGCGGACTGTACACAGCATCCTGACACAGTGC
CCAGGGCCTCCTGAAGGAGATCATCCTCGGACGACCTCAGCCAGCAAGGACAACACTCAAG
TCTGCTCTAGCGAATATGTGCCAGGCTGGAGGGGTGAAGTTACTCAGGAGCAACAAGAG
GCTGGGTGCCATCAGGGCCGGATGCTGGGGGCCACCAGAGCCACCGGGGATGTGCTCGTCT
TCATGGATGCCACTGCGAGTGCACCCAGGCTGGCTGGAGGCCCTCCTCAGCAGAATAGCT
GGTGACAGGAGCCAGTGGTATCTCCGGTGTAGATGTGATTGACTGGAAGACTTCCAGTA
TTACCCCTCAAAGGACCTGCAAGCTGGGGTGTGGACTGGAAGCTGGATTCCACTGGGAAC
CTTGCCAGAGCATGTGAGGAAGGCCCTCCAGTCCCCATAAGCCCCATCAGGAGCCCTGTG
GTGCCCGAGAGGGTGGCGATGGACAGACATTACTCCAAAACACTGGAGCGTATGACTC
TCTTATGTCGCTGCGAGGTGGTGAACCTCGAACACTGTCTTCAAGGCTGGCTGTGGTG
GCTCTGTTGAAATCCTCCCTGCTCTGGTAGGACACATCTACCAAAATCAGGATTCCAT
TCCCCCTCGACCAGGAGGCCACCTGAGGAACAGGGTTCGATTGCTGAGACCTGGCTGG
GTCATTCAAAGAACCTTCTACAAGCATAGCCCAGAGGCCCTCTCCTGAGCAAGGCTGAGA
AGCCAGACTGCATGGAACGCTTGCAAGCTGCAAAGGAGACTGGGTTGTCGGACATTCCACTGG
TTTCTGGCTAATGTCTACCCCTGAGCTGTACCCATCTGAACCCAGGCCAGTTCTGGAAA
GCTCCACAAACTGGACTTGGCTCTGTGCAAGACTGCCAGGCCAGCAAGTACCTGCAGCACACC
GTCCCCATGGTGGCTCTGCAAGTGCAGGCCAGCAACAGTACCTGCAGGCCAGTTCTGG
AGGAAGGAGATTCACTTGGCAGCCCACAGCACCTGTGCTTGTGCTGGCAGGAGCAGGT
GATTCTCAGAACACTGCACGGAGGAAGGCCATCCACCAGCAGCACTGGGACTTCCAGG
AGAATGGGATGATTGTCACATTCTTCTGGAAATGCATGGAAGCTGTGGTGCAAGAAAAC
ATAAAAGATTGTACCTGCGTCCGTGTGATGGAAAAGCCGCCAGCAGTGGCGATTGACCA
GATAAAATGCTGTGGATGAAACGATGAATGTCAATGTCAAGGAAAAGAGAATTGGCCATC
AAAATCCAGCTCCAAGTGAACGTTAAGAGCTTATATTTCATGAAAGCTGATCCTTTGTGT
GTGTGCTCCTGTGTTAGGAGAGAAAAAGCTATGAAAGAATATAGGAAGTTCTCCTT
TCACACCTTATTCATTGACTGCTGGCTGCTTA



U.S. PATENT AND TRADEMARK OFFICE

205/249

FIGURE 202

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73760
><subunit 1 of 1, 639 aa, 1 stop
><MW: 73063, pI: 6.84, NX(S/T): 2
MLLRKRYRHRPCRLQFLLLLMLGCVLMMVAMLHPPHTLHQTVTAQASKHSPEARYRLDFG
ESQDWVLEAEDEGEEYSPLEGLPPFISLREDQLLVAVALPQARRNQSQGRGGSYRLIKQPR
RQDKEAPKRDWGADEDGEVSEEEELTPFSLDPRGLQEALSARIPLQRALPEVRHPLCLQQHP
QDSLPTASVILCFHDEAWSTLLRTVHSILDTPRAFLKEIIILVDDLSQQGQLKSALSEYVAR
LEGVKLLRSNKRLGAIRARMLGATRATGDVLVFMDAHCECHPGWLEPLLSRIAGDRSRVVSP
VIDVIDWKTQYYPSKDLQRGVLDWKLDFHWEPLPEHVRKALQSPISPPIRSPVVPGEVVAMD
RHYFQNTGAYDSMSLRGGENLELSFKAWLCGGSVEILPCSRVGHIYQNQDSHSPLDQEATL
RNRVRIAETWLGSFKETFYKHSPEAFSLSKAEPDCMERLQLQRRRLGCRTFWFLANVPEL
YPSEPRPSFSGKLHNTGLGLCADCQAEGDILGCPMV LAPCSDSRQQQYLQHTSRKEIHFGSP
QHLCFAVRQEQQVILQNCTEEGLAIHQQHWDFQENGIVHILSGKCMEAVVQENNKDLYLRPC
DGKARQQWRFDQINAVDER
```

Signal peptide:

amino acids 1-28



206/249

FIGURE 203

CGCCAAGCATGCAGTAAAGGCTGAAAATCTGGGTACAGCTGAGGAAGACCTCAGAC**ATGGA**
GTCCAGGATGTGGCTGCGCTGCTGCTGTCCCACCTCCTCCCTCTGGCCACTGCTGTTGC
TGCCCCCTCCCACCGCCTGCTCAGGGCTTTCATCCTCCCTCGAACCCCCACCAGCCCCAGCC
CGCCCCCCCCTGTGCCAGGGGAGGCCCTCGGCCACGTATGTGCGTGTGGAGCGAGC
ACCTCCACCAAGCCGATCTCCTCGGGTCCAAGATCACGTCGGCAAGTCCTGCCTGGCACTG
CACCCCCAGCCACCCCATCAGGCTTGAGGAGGGGCCCTCATCCCAATACCCCTGGGCT
ATCGTGTGGGTCCCACCGTGTCTCGAGAGGATGGAGGGACCCCAACTCTGCCAATCCCGG
ATTCTGGACTATGGTTTGCAGCCCTCATGGGCTCGCAACCCCCACACCCCAACTCAGACT
CCATGCGAGGTGATGGAGATGGGTTATCCTGGAGAGGCACCTGCCACCCCTGGGCCATT
CTGTTGGGGGCCGTGGGAAGGTGTGGACCCCACTCTATGTCACAATTACCATCTCCAT
CATCATTGTTCTCGTGGCCACTGGCATCATCTCAAGTTCTGCTGGGACCGCAGCCAGAAGC
GACGCAGACCCCTCAGGGCAGCAAGGTGCCCTGAGGCAGGAGGAGGCCAGCAGCCACTGACA
GACCTGTCCCCGGCTGGAGTCAGTGTGCTGGGGCCTCGGGGACTCACCTACCCCAACCC
TGACCATGAGGAGCCCCGAGGGGACCCCGCTGGGATGCCCAACCCCAAGGGGCTCCAG
CCTTCCAGTTGAACCGG**TGA**GGGCAGGGCAATGGGATGGGAGGGCAAAGAGGGAAAGGCAAC
TTAGGTCTTCAGAGCTGGGGTGGGGGTGCCCTCTGGATGGTAGTGAGGAGGCAGGCAGC
CTCCCACAGCCCCCTGGCCCTCCCAAGGGGCTGGACAGCTCCTCTGGGAGGCACCC
CTTCTCCCAGTCTCAGGATCTGTCCTATTCTCTGCTGCCATAACTCCAACCTGCCC
TCTTGGTTTTCTCATGCCACCTGTCTAAAGACAACCTGCCCCTTAACCTTGATTCCC
CCTCTTGTCTTGAACCTCCCCTTCTATTCTGGCTACCCCTGGTTCTGACTGTGCCCTT
TCCCTCTCCTCTCAGGATCCCCCTGGTGAATCTGTGATGCCCAATGTTGGGTGCAGCC
AAGCAGGAGGCCAAGGGCCGGCACAGCCCCCATCCCAGTGGGTGGGCAGCTGTGGGA
GCTGGGCCACAGGGCTCTGGCTCTGCCCTTGACACACCACCGAACACTCCCCAGCC
CCACGGCAATCCTATCTGCTGCCCTCTGCAGGTGGGGCCTCACATATCTGTGACTTCG
GGTCCCTGTCCCCACCCCTGTGCACTCACATGAAAGCCTGACACTCACCTCACCT
AGGCCATTGCACACGCTCCTGCACCCCTCTCCCCGTCCATACCGCTCCGCTCAGCTGACTCT
CATGTTCTCGTCTCACATTGCACTCTCCTCTCCACATTCTGTGCTCAGCTCACTCAG
TGGTCAGCGTTCTGCACACTTACCTCTCATGTGCGTTCCGGCCTGATGTTGTGGTGG
TGTGCGCGTGTCACTCTCCCTCATGAACACCCACCCACCTCGTTCCGCAGCCCTGC
GTGCTGCTCCAGAGGTGGGTGGAGGTGAGCTGGGGCTCTGGGCCCTCATCGGTATGG
TCTCGTCCCATTCCACACCATTGTTCTCTGTCTCCCATCCTACTCCAAGGATGCCGGCA
TCACCCCTGAGGGCTCCCCCTGGGAATGGGTAGTGAGGCCAGACTTCACCCCAAGGCC
CTGCTAAAATCTGTTCTGACAGATGGGTTTGGGAGTCGCCTGCTGCACTACATGAGAA
AGGGACTCCCATTGCCCTCCCTTCTCCACAGTCCCTTTGTCTGTCTGCCCTGGCTG
TCTGTGTGTGCCATTCTCTGGACTTCAGAGCCCCCTGAGGCCAGTCCTCCCTCCAGCCT
CCCTTGGGCCTCCCTAACCTCCACCTAGGCTGCCAGGGACGGAGTCAGCTGGTTCAAGGCC
ATCGGGAGCTCTGCCCTCCAAGTCTACCCCTCCCTCCGGACTCCCTCTGTCCCCTCTTT
CCTCCCTCTTCCACTCTCCTCTTGTCTCCCTGGCTTCCCTCCCTGGCTCTAGGCT
CTTCCCTCTTCTACTGGTTTCCACCTCCCTCCCTTGTGGTGAATTACTGTG
GTGATATATATTTGTATTATCTCTTCTTGTGGTGAATTACTGTG
GGATGTAAGTTCAAAATTCAAAAGCCTTGCAAGATAA



207/249

FIGURE 204

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393
><subunit 1 of 1, 243 aa, 1 stop
><MW: 26266, pI: 8.43, NX(S/T): 1
MRPQGPAAQPQRLRGLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPAGV
PGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIA
ECTFTKMRNSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIYLDQGSPEMN
STINIHTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIIEELPK
```

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 195-217



208/249

FIGURE 205

GTAAACCAGCGCAGTCCTCCGTGCGTCCC GCCGCTGCCCTCACTCCC GGCCAGG**ATGG**
CATCCTGTCTGGCCCTGCGCATGGCGCTGCTGGTCTCCGGGTTCTGGCCCTGCGGTG
CTCACAGACGATGTTCCACAGGAGCCC GTGCCACGCTGTGGAACGAGCCGGCCGAGCTGCC
GTCGGGAGAAGGCCCGTGGAGAGCACCAGCCCCGGCCGGAGCCCGTGGACACCGGTCCCC
CAGCCCCCACC GTCGGCCAGGACCCGAGGACAGCACCGCGCAGGAGCGGCTGGACCAGGGC
GGCGGGTCGCTGGGGCCCGCGCTATCGCGGCCATCGT GATCGCCGCCCTGCTGGCACCTG
CGTGGT GCTGGCGCTCGTGGTCGCGCTGAGAAAGTTCTGCCTCCT**TGA**AAGCGAATAAA
GGGGCCCGCGCCGGCCGCGACTCGGCAAAAAAAA



209/249

FIGURE 206

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76398
><subunit 1 of 1, 121 aa, 1 stop
><MW: 12073, pI: 4.11, NX(S/T): 0
MASCLALRMALLLVSGVLAPAVLTDDVPQEPVPTLWNEPAELPSGEGPVESTSPGREPVDTG
PPAPTVAPGPEDSTAQERLDQGGGSLGPAGIAAIVIAALLATCVVLALVVVALRKFSAS
```

Important features of the protein:

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 91-110

Glycosaminoglycan attachment site.

amino acids 44-47

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 116-119

N-myristoylation site.

amino acids 91-96

**FIGURE 207**

GGCCGTTGGTGGTGC CGCGCTGAAGGGTGTGGCGAGCAGCGTC GTGGTTGCCGGCG
CGGGCCGGGACGGGC**ATG**CCCTGCTGCTGCCTGGTGTGCCTGACGGCGCGCTGGCCA
CGGCTGTCTGCACTGCCACAGCAACTTCTCCAAGAAGTTCTCCTTCTACCGCCACCATGTGA
ACTTCAAGTCCTGGTGGGTGGGCAGACATCCCCGTGTCAGGGCGCTGCTCACCGACTGGAGC
GACGACACGATGAAGGAGCTGCACCTGCCATCCCCGCCAAGATCACCCGGGAGAAGCTGGA
CCAAGTGGCGACAGCAGTGTACCAAGATGATGGATCAGCTGTACCAAGGGAAAGATGTACTTCC
CCGGTATTCCCCAACGAGCTGCAGAACATCTCCGGGAGCAGGTGCACCTCATCCAGAAC
GCCATCATCGAAAGGCACCTGGCACCCAGGCAGCTGGGAGGAGGGCAGCTCTCCAGGGAGGG
ACCCAGCCTAGCACCTGAAGGATCAATGCCATCACCCCGCGGGGACCTCCCC**TAA**GTAGCCC
CCAGAGGCCTGGGAGTGTGCCACCGCCCTCCCTGAAGTTGCTCCATCTCACGCTGGGG
GTCAACCTGGGACCCCTCCCTCCGGGCCATGGACACACATACATGAAAACCAGGCCGCAT
CGACTGTCAGCACCGCTGTGGCATCTTCAGTACGAGACCATCTCCTGCAACAACTGCACAG
ACTCGCACGTCGCCTGCTTGCTATAACTGCGAGTAGGGCTCAGGCATCACACCCACCGT
GCCAGGGCCCTACTGTCCCTGGGTCCCAGGCTCTCCTGGAGGGGCTCCCCGCTTCCAC
CTGGCTGTCATCGGTAGGGCGGGCGTGGTTCAAGGGCGCACCACCTCCAAGCCTGTGT
CCCACAGGTCTCGCGCAGTGGAAAGTCAGCTGTCCAGGGCCTCCTGAACACTACATAAAAC
TGGCACAAGTAAGTCCCCTCTCAAACCAACACAGGCAGTGTGTATGTGAGCACCTCGTG
GGTAGTATGTGTGGGGCACAGGCTGGCTCCCTCAGCTCCACGTCTTAGAGGGGCTCCGA
GGAGGTGGAACCTCAACCCAGCTCTCGCAGGAGGGCGCTGCAGTCCTTCTCCCTCAAAG
GTCTCCGACCCTCAGCTGGAGGCAGGCGGCATCTTCTAAAGGGTCCCCTAGGGCTGGTCC
ACCCCATCCCAGGTCTGTGGTCAGAGCCTGGGAGGGTCCCTACGATGGTTAGGGTGCCTC
ATGGAGGGGCTGACTGCCACATTGCCCTTCAGACAGGACACGAGCATGAGGTAAGGCCGC
CCTGACCTGGACTTCAGGGGAGGGGTAAGGGAGAGAGGAGGGGGCTAGGGGCTCCCT
AGATCAGTGGGGCACTGCAGGTGGGCTCCCTACCTGGACACCTGCTGGATGTCAC
CTCTGCAACCACACCCATGTGGTGGTTCATGAACAGACCACGCTCCTCTGCCCTCTCCTGG
CCTGGACACACAGAGCCACCCGGCCTTGTGAGTGACCCAGAGAAGGGAGGCCTCGGAGA
AGGGGTCTGTAAGCCAACACCAGCGTGCCCGGCTGCACACCCCTCGGACATCCCAGGC
ACGAGGGTGTGGATGTGGCACACATAGGACCACACGTCCCAGCTGGAGGAGAGGCCT
GGGGCCCCCAGGGAGGGAGGCAGGGGTGGGGACATGGAGAGCTGAGGCAGCCTCGTCTCC
CCGCAGCCTGGTATGCCAGCCTTAAGGTGTCTGGAGCCCCACACTTGGCCAACCTGACCT
TGGAAAGATGCTGCTGAGTGTCTCAAGCAGCACTGACAGCAGCTGGCCTGCCAGGGCAAC
GTGGGGCGGAGACTCAGCTGGACAGCCCCCTGCCTGTCACTCTGGAGCTGGCCTGCTGCTGC
CTCAGGACCCCTCTCCGACCCGGACAGAGCTGAGCTGGCCAGGGCAGGAGGGCGGGAGG
GAGGGAATGGGGTGGCTGTGCGCAGCATTAGCGCCTGGCAGGTCCGCAGAGCTGCGGGA
TGTGATTAAAGTCCCTGATGTTCTC



211/249

FIGURE 208

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76399

><subunit 1 of 1, 157 aa, 1 stop

><MW: 17681, pI: 7.65, NX(S/T): 1

MALLLCLVCLTAALAHGCLHCHSNFSKKFSFYRHHVNFKSWWVGDI

ELHLAIPIAKITREKLDQVATAVYQMMMDQLYQGKMYFPGYFPNELRNIFREQVHLIQNAAIER

HLAPGSWGGQLSREGPSLAPEGSMPSPRGDLP

Signal peptide:

amino acids 1-15



212/249

FIGURE 209

AGCAGGAGCAGGAGAGGGACAATGGAAGCTGCCCGTCCAGGTTCATGTTCTCTTATTCT
CCTCACGTGTGAGCTGGCTGCAGAAGTTGCTGCAGAAGTTGAGAAATCCTCAGATGGCCTG
GTGCTGCCAGGAACCCACGTGGCTCACAGATGTCCCAGCTGCCATGGAATTCAATTGCTGCC
ACTGAGGTGGCTGTCATAGGCTTCTTCAGGATTAGAAATACCAGCAGTGCCACTCCA
TAGCATGGTCAAAAATTCCCAGGGCGTGTCAATTGGGATCAGCACTGATTCTGAGGTTCTGA
CACACTACAAACATCACTGGAACACCATCTGCCTCTTCGCCTGGTAGACAATGAACAACTG
AATTAGAGGACGAAGACATTGAAAGCATTGATGCCACAAATTGAGCCGTTCAATTGAGAT
CAACAGCCTCCACATGGTACAGAGTACAACCTGTGACTGTGATTGGGTTATTCAACAGCG
TAATTCAATTGATTCCTCCTGATAATGAACAAAGGCCTCCCCAGAGTATGAAGAGAACATG
CACAGATAACCAGAAGGCAGCCAAGCTCTTCAGGGGAAGATTCTCTTATTCTGGTGGACAG
TGGTATGAAAGAAAATGGGAAGGTGATATCATTTCAAACTAAAGGAGTCTCAACTGCCAG
CTTGGCAATTACAGACTCTAGATGACGAGTGGATAACTGCCACAGCAGAAGTTCC
GTAGAGCATGTGCAAAACTTTGTGATGGATTCTAAGTGGAAAATTGTTGAAAGAAAATCG
TGAATCAGAAGGAAAGACTCCAAAGGTGGAACTGACTTCTCCTGGAACTACATATGGCC
AAGTATCTACTTATGCAAAGTAAAAAGGCACAACTCAAATCTCAGAGACACTAAACAAACAG
GATCACTAGGCCTGCCAACACACACACACACAGCAGTCACACACGCACGCACCGTGCACAC
ACACACCGCACACACACACACACAGAGCTCATTCTGTCTTAAATCTGTTCTC
TTCTCCTCTTAAATTCAATCCTCACTCCCTATCCAATTCTCTTATCGTCATT
CATACTCTGTAAGCCCCTGTAACACACACAGCTGACTCAAGGCTTAAAGAGACTCACTGTGATG
CCTCTATGAAAGAGAGGCATTCTAGAGAAAGATTGTTCAATTGTCATTAAATATCAAGT
TTGTATACTGCACATGACTTACACACACATAGTTCTGCTTTAAGGTTACCTAAGGGT
TGAAACTCTACCTCTTCAAAACACCTTGTGAAATTGTCTTTGCCAGAAGTTAAAGGCTGCTCCAAGTC
CCTGAACTCAGCAGAAATAGACCATGTTGAAAACCTCCATGCTGGTTAGCATCTCCAACCTCC
TATGTAATCAACAACCTGCATAATAAAAGGCAATCATGTTATA



213/249

FIGURE 210

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76401
><subunit 1 of 1, 273 aa, 1 stop
><MW: 30480, pI: 4.60, NX(S/T): 1
MEAAPSRFMFLLFLLTCELAAEVAEVEKSSDGPAGAAQEPTWLTDVPAAMEFIAATEVAVIG
FFQDLEIPAVPILHSMVQKFPGVSGFGISTDSEVLTHYNITGNTICLFRFLVDNEQLNLEDEDI
ESIDATKLSRFIEINSLHMVTEYNPVTIVIGLFNSVIQIHLLIMNKASPEYEENMHRYQKAA
KLFQGKILFILVDGMKENGKVISFFKLKESQLPALAIYQTLDEWDTLPTAEVSVEHVQNF
CDGFLSGKLLKENRESEGKTPKVEL
```

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 143-162



214/249

FIGURE 211

GGAGAGCCGCGGCTGGACCGAGTGGGGAGCGCGCGTGGAGGTGCCACCCGGCGCGGGTG
GCGGAGAGATCAGAAGCCTCTTCCCCAAGCCGAGCCAACCTCAGCGGGGACCCGGGCTCAGG
GACGCGGCGGGCGCGCGACTGCAGTGGCTGGACGATGGCAGCGTCCGCCGGAGCCGGG
GCGGTGATTGCAGCCCCAGACAGCCGGCGCTGGCTGTGGTCGGTGTGGCGGCCGGCTTGG
GCTCTTGACAGCTGGAGTATCAGCCTTGAAGTATAACGCCAAAAGAAATCTCGTGGCAA
ATGGTACACAAGGGAAGCTGACCTGCAAGTCAAGTCTACTAGTACGACTGGCGGGTTGACC
TCAGTCTCCTGGAGCTCCAGCCAGAGGGGGCGACACTACTGTGTGTTTCCACTACTC
CCAAGGGCAAGTGTACCTTGGATTATCACCATTAAAGACAGAACAGCTGGGCTGGAG
ACCTTGACAAGAAAGATGCATCAATCAACATAGAAAATATGCAGTTATACACAATGGCAC
TATATCTGTGATGTCAAAAACCCTCTGACATCGTGTCCAGCCTGGACACATTAGGCTCTA
TGTCGTAGAAAAAGAGAATTGCCTGTGTTCCAGTTGGTAGTGGTGGCATAGTTACTG
CTGTGGCCTAGGTCTCACTCTGCTCATCAGCATGATTCTGGCTGTGCTCTATAGAAGGAAA
AACTCTAAACGGGATTACACTGGCTGCAGTACATCAGAGAGTTGTACCAGTTAACAGGC
TCCTCGGAAGTCCCCCTCCGACACTGAGGGCTTGTAAAGAGTCTGCCTCTGGATCTCACC
AGGGCCCAGTCATATATGCACAGTTAGACCACTCCGGCGGACATCACAGTGACAAGATTAAC
AAGTCAGAGTCTGGGTATGCGGATATCCGAAAGAATTAAGAGAACACATAC
CTCAGCAAGAAACAAACCAACTGGACTCTCGTCAGAAAATGTAGCCCATTACACATGT
AGCCTTGGAGACCCAGGCAAGGACAAGTACACGTGTACTCACAGAGGGAGAGAAAGATGTGT
ACAAAGGATATGTATAAATATTCTATTAGTCATCCTGATATGAGGAGCCAGTGTGATGA
TGAAAAGATGGTATGATTCTACATATGTACCCATTGTCTTGCTGTTTGACTTCTTTTC
AGGTCAATTACAATTGGAGATTCAGAAACATTCTTCAACCACATTAGAAATGGTTG
CCTTAATGGAGACAATAGCAGATCCTGTAGTATTCCAGTAGACATGGCCTTTAATCTAAG
GGCTTAAGACTGATTAGTCTTAGCATTACTGTAGTTGGAGGATGGAGATGCTATGATGGAA
GCATACCCAGGGTGGCCTTACAGTACATTGAGGAGCTGCTGCGCTTTAAAG
AATACCCATTGGCTATGCCACTTGAAAACAATTGAGAAGTTTTGAAGTTTCTCACT
AAAATATGGGCATTGTTAGCCTACATGTTGTAGACTACTTAAGTTGCACCCCTG
AAATGTGTCATATCAATTCTGGATTCAATAAGCAAGATTAGCAAAGGATAATGCCAAG
GTCACCTCATTCTGGACACAGTTGGATCAAACTGATTAAGTAGAAAATCCAAGCTTGCTT
GAGAACTTTGTAACGTGGAGAGTAAAAAGTATCGGTTTA



215/249

FIGURE 212

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76510
><subunit 1 of 1, 269 aa, 1 stop
><MW: 29082, pI: 9.02, NX(S/T): 3
MAASAGAGAVIAAPDSRRWLWSVLAAALGLLTAGVSALEVYTPKEIFVANGTQGKLTCKFKST
TSTTGGLTSVSWSFQPEGADTTVSFFHYSQGQVYLGNYPPFKDRISWAGDLDKKDASINEN
MQFIHNGTYICDVKNPPDIVVQPGHIRLYVVEKENLPVFPVVVGIVTAVVLGLTLLISMIL
LAVLYRRKNSKRDYTGCSTSESLSPVKQAPRKSPSDTEGLVKSLPSGSHQGPVIYAQLDHSG
GHHSDKINKSESVVYADIRKN
```

Signal peptide:

amino acids 1-37

Transmembrane domain:

amino acids 161-183



216/249

FIGURE 213

GGCGGCTGTGCAGAGACGCC **ATGT** ACCGGCTCCTGTCAGCAGTGACTGCCGGCTGCCGCC
CCCGGGGGCTTGGCCTCAAGCTGCGGACGACGCCGGTCCATCAGCGCCGCCGGCTGCCGCC
TCTCGGCCACGGCTGGGTGGGGCTCGGGCTGGGCTGGGCTGGCGCTCGGGTGAAGC
TGGCAGGTGGGCTGAGGGCGCGCCCCGGCGCAGTCCCCCGCGCCCCGACCTGAGGCG
TCGCCTCTGGCGAGCCACAGGAGCAGTCCTCGCCCCGTGGTCTCGCAGACCCGGC
GCCGCCCTGCTCCAGGTGCTCGCCAGAGCATCGAGAGCAGCCGCACCTGCTGCACAGGA
TCAAGGATGAGGTGGCGCACCGGCATAGTGGTTGGAGTTCTGTAGATGGAAAAGAAGTC
TGGTCAGAAGGTTAGGTTATGCTGATGTTGAGAACCGTGTACCATGTAAACCAGAGACAGT
TATGCGAATTGCTAGCATCAGAAAAGTCTCACCATGGTTGCTCTGCCAAATTGTGGGAAG
CAGGGAAACTGGATCTTGATATTCCAGTACAACATTATGTTCCGAATTCCCAGAAAAGAA
TATGAAGGTGAAAAGGTTCTGTACAACAAGATTACTGATTCCCATTAAGCCTGAAGATGA
TCATTATGAAAAGGACATAAAAAGGTGAAAGAAGAGAAAGCTTATAAAGCCTGAAGATGA
TGAAAGAGAATGTTGCATTGAGCAAGAAAAAGAAGGCAAAGTAATGAAAAGAATGATT
ACTAAATTAAAACAGAGCAGGAGAATGAAGCCAATGCCGAATTCAAAACCTGGCAAGAA
AAAGAATGATTGAAACAAGGCAATTATATTGAGAGAAAAGTTGAAAATTCAATTGAAT
CCCTAAGATTATTAAAAATGATCCTTGTCTTCAAACCTGGTAGTCAGTTTGATTCA
ACTTTGGCTATAACCCTACTGGCAGCCATAGTAGAGAGAGCTCAGGATGAAATATTGGA
CTATATGCAGAAAATATTCCATGACTGGATATGCTGACGACTGTGCAGGAAGAAAACGAGC
CAGTGATTACAATAGAGCAAGG**TAA**ATGAATACTCTGCTGTCTAGCTATATCGCATC
TTAACACTATTATTAAATTAAAAGTCAAATTCTTGTGTTCCATTCAAAATCAACCTGC
CACATTGGAGCTTCTACATGTCTGTTCTCATCTGAAAGTGAAGGAAGTAAAACA
TGTTTATAAAAGTAAAAAAA



217/249

FIGURE 214

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76522
><subunit 1 of 1, 373 aa, 1 stop
><MW: 41221, pI: 8.54, NX(S/T): 0
MYRLLSAVTARAAAPGGLASSCGRRGVHQAGLPPLGHGWVGGLGLGLALGVKLAGGLRG
AAPAQSPAAPDPEASPLAEPQEQSLAPWSPQTAPPSCRCFARAIESSRDLLHRIKDEVGA
PGIVVGVSVDGKEVWSEGLGYADVENRVPCKPETVMRIASISKSLSLTVALAKLWEAGKLDLD
IPVQHYVPEFPEKEYEGEKVSVTLLISHLSGIRHYEKDIKKVKEEKAYKALKMMKENVAF
EQEKEGKSNEKNDFTKFKTEQENEAKCRNSKPGKKNDFEQGELYLREKFENSIESRLFKN
DPLFFKPGSQFLYSTFGYTLAAIVERASGCKYLDYMQKIFHDLDMLTTVQEENEPVIYNRAR
```

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 39-60



218/249

FIGURE 215

GTGACACTATAGAAGAGCTATGACGTCGCATGCACCGTACGTAAGCTCGGAATTGGCTCG
AGGCTGGTGGAAAGAAGCCGAGATGCGGGCAGCCAGCGCTGGGCAACCCGGCTGCTCCTGC
TCTTGCTGATGGCGGTAGCAGCGCCAGTCGAGCCCAGGGCAGCGGCTGCCGGCCGGACT
GGTGCAGGGCTGGGGCGGAAGGTCGAGAGGGCGAGGCTGTGGCACGGTGGGCTGCT
GCTGGAGCACTCATTTGAGATCGATGACAGTGCCAACTTCCGAAGCAGGGCTCACTGCTCT
GGAACCAGCAGGATGGTACCTTGTCCCTGTACAGCGGCAGCTCAGCGAGGAGGAGCAGGGC
CGACTCCGGATGTGGCAGCCCTGAATGGCCTGTACCGGGTCCGGATCCCAAGGCGACCCGG
GGCCCTGGATGGCCTGGAAGCTGGCTATGTCTCCTCCTTGTCCCTGCGTGCTCCCTGG
TGGAGTCGCACCTGTCGGACCAGCTGACCTGCACGTGGATGTGGCCGGAACGTGGTGGC
GTGTCGGTGGTACGCACCCGGGGCTGCCGGGGCATGAGGTGGAGGACGTGGACCTGG
GCTGTTCAACACCTCGGTGCAGCTGCAGCCGCCACACAGCCCCAGGCCCTGAGACGGCG
CCTTCATTGAGCGCCTGGAGATGGAACAGGCCAGAAGGCCAAGAACCCCCAGGAGCAGAAG
TCCTTCTCGCAAATACTGGATGTACATCATTCCCGTGTCCCTGTTCTCATGATGTCAGG
AGCGCCAGACACCGGGGCCAGGGTGGGGTGGGGGTGGTAGTGGCC
TTTGCTGTGCCACCCCTCCCTGTAAGTCTATTAAAAACATCGACGATACTTGAATGTG
TGAACGTTTGAAAAGCTACAGCTTCCAGCAGCCAAAGCAACTGTTGTTGGCAAGACGG
TCCTGATGTACAAGCTTGATTGAAATTCACTGCTACITGATACGTTATTCAAGAACCCAAG
GAATGGCTGTCCCCATCCTCATGTGGCTGTGGAGCTCAGCTGTGTGTGGCAGTTAT
TAAACTGTCCCCAGATCGACACGCAAAAAAAA



219/249

FIGURE 216

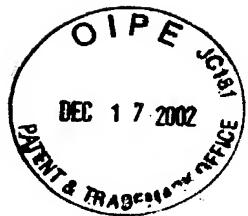
```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76529
><subunit 1 of 1, 269 aa, 1 stop
><MW: 28004, pI: 5.80, NX(S/T): 1
MAAASAGATRLLLLLMAVAAPS RARGSGCRAFTGARGAGAEGREGEACGTVGLLLEHSFEI
DDSANFRKRGSLIWNQQDGTLSQRQLSEEERGRLRDVAALNGLYRVRI PRRPGALDGLEA
GGYVSSFVPACSLVESHLSDQLTLHVDVAGNVGVSVTHPGGCRGHEVEDVDLELFNTSVQ
LQPPTTAPGPETAAFIERLEMEQAQKAKNPQEOKSFFAKYW MYII PVVLFLMMMSGAPDTGGQ
GGGGGGGGGGGGSGLCCVPPSL
```

Signal peptide:

amino acids 1-24

Transmembrane domain:

amino acids 226-243



220/249

FIGURE 217

GGAGCGCTGCTGGAACCCGAGCCGGAGCCACAGCAGGGAGGGTGGCCTGGCGGCCT
GGAGCCGGACGTGTCCGGGGGTCCCCGCAGACCGGGCAGCAGGTGTCCTGGGGCCACC
ATGCTGGTGACTGCCTACCTGCTTTGTAGGCCTCCTGGCCTCCTGCCCTGGGCTGGAACCT
GTCAAGATGCCGGCTAAACCCCCTGGAAGGGCCTGCAGCAATCCCTCCTCCTCGGTTTC
AACTGGACTTCTATCAGGTCTACTCCTGCCCTGGCAGCTGATTGGCTTCAGGCCCTAC
CTCTATAAAACTCTACCAAGCATTACTACTTCCTGGAAGGTCAAATTGCCATCCTCTATGTCTG
TGGCCTTGCCTCTACAGTCCTCTTGGCCTAGTGGCCTCCCTGTGGATTGGCTGGTC
GCAAGAATTCTTGTGTCCCTCTTCCCTGACTTACTCACTATGCTGCTAACCAAACCTCT
CAAGACTACTTGTGCTGCTAGTGGGCGAGCACTGGTGGCTGTCCACAGCCCTGCTCTT
CTCAGCCTTCGAGGCCTGGTATATCCATGAGCACGTGGAACGGCATGACTCCCTGCTGAGT
GGATCCCAGCTACCTTGCTCGAGCTGCCTCTGGAACCATGTGCTGGCTGTAGTGGCAGGT
GTGGCAGCTGAGGCTGTAGCCAGCTGGATAGGGCTGGGCCTGTAGGCCCTTGTGGCTGC
CATCCCTCTGGCTCTGGCAGGGGCCTGGCCCTCGAAACTGGGGGAGAACTATGACC
GGCAGCGTGCCTCTCAAGGACCTGTGCTGGAGGCCTGCGCTGCCTCCTGCGACCGCCGC
GTGCTGCTGGCACCATAAGCTCTATTGAGAGTGTATCTTGTGCTTGTGCTTCT
CTGGACACCTGTGCTGGACCCACACGGGCCCCCTGGCATTATCTTCTCCAGCTTGTGCT
CAGCCAGCCTGCTGGCTCTCCCTGTACCGTATGCCACCTCCAAGAGGTACCACTTCAG
CCCATGCACCTGCTGTCCCTGCTGTGCTCATCGTCGTCTCTCTCTTGTGACTTT
CTCTACCAGCCCAGGCCAGGAGAGTCCGGTGGAGTCCTCATAGCCTTCTACTTATTGAGT
TGGCTTGTGGATTATACTTCCCAGCATGAGCTCCTACGGAGAAAGGTGATCCCTGAGACA
GAGCAGGCTGGTGTACTCAACTGGTCCGGTACCTCTGCACACTGGCTGCCTAGGGCT
CCTTGTCTCCATGACAGTGATCGAAAAACAGGCACTCGGAATATGTTGCTCAGCATTTGCTCTG
CTGTCATGGTGTGATGGCTCTGCTGGCAGTGGTGGACTCTCACCGTGGTAAGGCATGATGCT
GAGCTGCGGGTACCTCACCTACTGAGGAGCCCTATGCCCTGAGCTG**TAA**CCCCACTCCAG
GACAAGATAGCTGGGACAGACTCTGAATTCCAGCTATCCGGATTGTACAGATCTCTGT
GACTGACTTGTGACTGTCCCTGTGGTTCTCCTGCCATTGCTTGTGTTGGAGGACATGA
TGGGGGTGATGGACTGGAAAGAAGGTGCCAAAGTCCCTCTGTGTTACTCCCATTAGAAA
ATAAACACTTTAAATGATCAAAAAAAAAAA



1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20

221/249

FIGURE 218

MLVTAYLAFVGLLASCLGLELSRCRAKPPGRACSNPSFLRFQLDFYQVYFLALAADWLQAPY
LYKLYQHYYFLEGQIAILYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTYSLCCLTKLS
QDYFVLLVGRALGGLSTALLFSAFEAWYIHEHVERHDFPAEWIPATFARA_AFWNHVLA
VAGVAEEAVASWIGLGPVAPFVAAIPLLALAGALALRNWGENYDRQRAFSRTCAGGLRCLLSDR
VLLLGTIQALFESVIFIFVFLWTPVLDPHGAPLGIIFFSSFMAASLLGSSLYRIATSKRYHLQ
PMHLLSLAVLIVVFSLFMLTFSTSPGQESPVESFIAFLIELACGLYFPSMSFLRRKVIPET
EQAGVLNWFRVPLHSLACLGLLVLHDSDRKTGTRNMFSICSAVMVMALLAVVGLFTVVRHDA
ELRVPSPTEEPYAPEL

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 41-55, 75-94, 127-143, 191-213, 249-270, 278-299,
314-330, 343-359, 379-394, 410-430



222/249

FIGURE 219

GCGACGCGCGGGCGGGCGAGAGGAAACGCAGGCCGGCCGGCCGGCCCTGGAG**ATG**
GTCCCCGGCGCCGCGGGCTGGTGTCTCGTCTGGCTCCCCGCGTGCCTCGCGGCCA
CGGCTTCGTATCCATGATTATTGTACTTCAGTGCTGAGTCCTGGGACATTGATACA
TCTTCACAGCCACACCTGCCAACGGACTTGGTGGTATCTTCACACAAGGTATGAGCAGATT
CACCTTGCCCCGCTGAACCTCCAGAGGCCTGCAGGGAACTCAGCAACGGTTCTTCATCCA
GGACCAGATTGCTCTGGTGGAGAGGGGGCTGCTCCTCTCCAAGACTCGGGTGGTCC
AGGAGCACGGCGGGCGGGCGGTGATCATCTCTGACAAACGCAGTTGACAATGACAGCTTCTAC
GTGGAGATGATCCAGGACAGTACCCAGCGCACAGCTGACATCCCCGCCCTTCTGCTCGG
CCGAGACGGCTACATGATCCGCCCTCTGGAACAGCATGGCTGCCATGGCCATCATT
CCATCCCAGTCAATGTCACCAGCATCCCCACCTTGAGCTGCAACCGCCCTGGACCTTC
TGGTAGAAGAGTTGCTACTTGAATTGGAGATAGCATCTGGGACAAGTGGAGCCAGGTAGAGGA
AGGAATTGGCTACTTGAATTGGAGATAGCATCTGGGACAAGTGGAGCCAGGTAGAGGA
AAAGGGTTGGCGTTGCTAGGCTGAAAGGGAAAGCCACACCCTGGCCTCCCTCCCCAGG
GCCCAAGGGTGTCTCATGCTACAAGAAGAGGCAAGAGACAGGCCAGGGCTTCTGGCTA
GAACCCGAAACAAAAGGAGCTGAAGGCAGGTGGCCTGAGAGCCATCTGACCTGTCACACT
CACCTGGCTCCAGCCTCCCCACCCAGGGTCTCTGCACAGTGACCTCACAGCAGTTGG
AGTGGTTAAAGAGCTGGTGGACTCAATAACCCCTCACTGACTTTAGCAATAAA
GCTTCTCATCAGGGTTGCAAAAAAAAAAAAAAA



2025 RELEASE UNDER E.O. 14176

223/249

FIGURE 220

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76532
><subunit 1 of 1, 188 aa, 1 stop
><MW: 21042, pI: 5.36, NX(S/T): 2
MVPGAAGWCCLVLWLPACVAAHGFRIGHDYLYFQVLSPGDIRYIFTATPAKDFGGIFHTRYEQ
IHLVPAEPPEACGELSNGFFIQDQIALVERGGCSFLSKTRVVQEHGGRAVIISDNAVDNDSF
YVEMIQDSTQRTADIPALFLLGRDGYMIRRSLEQHGLPWAIISIPVNVTSIPTFELLQPPWTFW
```

Signal peptide:

amino acids 1-20



2025 RELEASE UNDER E.O. 14176

224/249

FIGURE 221

TCTGCCTCCACTGCTCTGTGCTGGGATCATGGAACTTGCACTGCTGTGGCTGGTGGTGA
TGGCTGGTGTGATTCCAATCCAGGGCGGGATCCTGAACCTGAACAAGATGGTCAAGCAAGTG
ACTGGGAAAATGCCCATCCTCTCCTACTGGCCCTACGGCTGTCAGTGCAGACTAGGTGGCAG
AGGCCAACCCAAAGATGCCACGGACTGGTGTGCCAGACCCATGACTGCTGCTATGACCACC
TGAAGACCCAGGGGTGCCATCTACAAGGACAACAACAAAAGCAGCATACTTGTATGGAT
TTATCTCAACGCTATTGTTAATGGCTGTGTTAATGTGATCTATCTGGAAAATGAGGACTC
CGATAAAAGCTATTACTAWTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAA



225/249

FIGURE 222

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76538

><subunit 1 of 1, 116 aa, 1 stop

><MW: 12910, pI: 6.41, NX(S/T): 1

MELALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCCHCGLGGRGQPKDATDW
CCQTHDCCYDHLKTQGCGIYKDNNKSSIHCMDLSQRYCLMAVFVNVIYLENEDSE

Important features of the protein:

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 1-24

N-glycosylation site.

amino acids 86-89

N-myristoylation sites.

amino acids 20-25, 45-50

Phospholipase A2 histidine active site.

amino acids 63-70



226/249

FIGURE 223

CTCGCTTCTTCCTCTGGATGGGGGCCAGGGGCCAGGAGAGTATAAAGGCATGTGGAG
GGTGCCCGACAACCAGACGCCAGTCACAGCGAGAGCCCTGGG**ATG**CACCGGCCAGAGG
CCATGCTGCTGCTCACGCTTGCCTCCTGGGGCCCACCTGGCAGGAAAGATGTAT
GGCCCTGGAGGAGGCAAGTATTCAGCACCCTGAAGACTACGACCATGAAATCACAGGGCT
GCGGGTGTCTGTAGGTCTTCCTGGTAAAAAGTGTCCAGGTGAAACCTGGAGACTCCTGGG
ACGTGAAACTGGGAGCCTAGGTGGAAATACCCAGGAAGTCACCCCTGCAGCCAGGCGAACATAC
ATCACAAAAGTCTTGTGCCTCCAAGCTTCCTCCGGGTATGGTCATGTACACCAGCAA
GGACCGCTATTCTATTTGGAAAGCTTGATGCCAGATCTCCTGCCTACCCAGCCAAG
AGGGGCAGGTGCTGGTGGCATCTATGCCAGTATCAACTCCTGGCATCAAGAGCATTGGC
TTTGAATGAAATTATCCACTAGAGGAGCCGACCACTGAGCCACCAAGTTAATCTCACATACTC
AGCAAACTCACCCGTGGTCGC**TAG**GGTGGGTATGGGCCATCCGAGCTGAGGCCATCTGT
GTGGTGGTGGCTGATGGTACTGGAGTAAGTGAATCGGGACGCTGAATCTGAATCCACCAATA
ATAAAAGCTTCTGCAGAAAA



227/249

FIGURE 224

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76541
><subunit 1 of 1, 178 aa, 1 stop
><MW: 19600, pI: 5.89, NX(S/T): 1
MHRPEAMLLLTLALLGGPTWAGKMYGPGGGKYFSTTEDYDHEITGLRVSVGLLLKVSVQVK
LGDSWDVKGALGGNTQEVTLQPGEYITKVFVAFQAFLRGMVMYTSKDRYFYFGKLDGQISS
AYPSQEGQVLVGIYGQYQLLGIKSIGFEWNYPLEEPTTEPPVNLTYSANSPVGR
```

Signal peptide:

amino acids 1-22



228/249

FIGURE 225

GCTGAGCGTGTGCGCGGTACGGGGCTCTCCTGCCTCTGGGCTCCAACGCAGCTCTGTGGCT
GAAC TGGGTGCTCATCACGGGA ACTGCTGGGCTATGGAATACAGATGTGGCAGCTCAGGTAG
CCCCAAATTGCCTGGAAGAATAACATCATGTTTTCGATAAGAAGAAATTGTAGGATCCAGTT
TTTTTTTAACCGCCCCCTCCCCACCCCCAAAAAAACTGTAAAGATGCAAAAACGTAATAT
CCATGAAGATCCTATTACCTAGGAAGATTGATTTGCTGCGAATGCGGTGTTGGGATT
TATTGTTCTGGAGTGTCTGCGTGGCTGGCAAAGAATAATGTTCCAAAATCGGTCCATCT
CCCAAGGGTCCAATTTCCTGGGTGTCAGCGAGCCCTGACTCACTACAGTCAGCTG
ACAGGGCTGTCACTGCAACTGGCCCTAACGCCAAAGCAGCTAACCTAGGACGACCTTGAA
CAATACAAAGGATGGTTCAATGTAATTAGGCTACTGAGCGGATCAGCTGTAGCACTGGTT
ATAGCCCCACTGTCTTACTGACAATGCTTCTTGCGAACGAGGATGCCCTAAGGGCTG
TAGGTGTGAAGGCAAATGGTATATTGTGAATCTCAGAAATTACAGGAGATACCCTCAAGTA
TATCTGCTGGTTGCTTAGGTTGTCCTCGCTATAACAGCCTCAAAAACCTTAAGTATAAT
CAATTAAAGGGCTCAACCAGCTCACCTGGCTATACTTGACCATAACCATATCAGCAATAT
TGACGAAAATGCTTTAATGGAATACCGCAGACTCAAAGAGCTGATTCTTAGTCCAATAGAA
TCTCCTATTTCTAACAAATACCTCAGACCTGTGACAAATTACGGAACTTGGATCTGTC
TATAATCAGCTGCATTCTGGGATCTGAACAGTTGGGGCTTGCGGAAGCTGCTGAGTT
ACATTACGGTCTAACCCCTGAGAACCATCCCTGTGCGAATATTCCAAGACTGCCGCAACC
TGGAACTTTGGACCTGGGATATAACCGGATCCGAAGTTAGCCAGGAATGTCTTGCTGGC
ATGATCAGACTCAAAGAACTTCACCTGGAGCACAATCAATTTCAGCTCAACCTGGCCCT
TTTCCAAGGTTGGTCAGCCTTCAGAACCTTACTTGCAGTGGAAATAAAATCAGTGTCTAG
GACAGACCATGTCCGGACCTGGAGCTCCTACAAAGGCTTGTGATTATCAGGCAATGAGATC
GAAGCTTCAGTGGACCCAGTGTGTTCCAGTGTGTCCTGAATCTGCAGCGCCTCAACCTGGA
TTCCAACAAGCTCACATTATTGGTCAAGAGATTGGATTCTGGATATCCCTCAATGACA
TCAGTCTGCTGGGAATATATGGGAATGCAAGCAGAAATATTGCTCCCTGTAAACTGGCTG
AAAAGTTAAAGGTCTAAGGGAGAATAACATTATCTGTGCCAGTCCAAAGAGCTGCAAGG
AGTAAATGTGATCGATGCAGTGAAGAAACTACAGCATCTGTGCCAGTCCAAAGAGACTACAGAGAGGT
TTGATCTGCCAGGGCTCTCCAAAGCCGACGTTAACGCCAGCTCCCAAGGCCAGAGACCAG
GAGAGCAAACCCCTTGGCCCCGACGGTGGAGCCACAGAGCCGGCCAGAGACCAG
TGACGCCGAGCACATCTTCCATAAAATCATCGGGCAGCGTGGCGCTTCTGTCCG
TGCTCGTCATCCTGCTGGTTATCTACGTGTCAAGCGGTACCTCGAGCATGAAGCAG
CTGCAGCAGCGCTCCCTCATGCGAAGGCACAGGAAAAAGAAAAGACAGTCCCTAAAGCAAAT
GAACCCCAGCACCCAGGAATTATGTAGATTATAAACCCACCAACACGGAGACCAGGAGA
TGCTGCTGAATGGGACGGGACCCCTGCACCTATAACAAATCGGGCTCCAGGGAGTGTGAGGTA
TGAACCATTGTGATAAAAGAGCTCTAAAGCTGGAAATAAGTGGTGTATTGAAC
TGGTGACTATCAAGGGAACCGCATGCCCTCCCTCCCTCTCCCTCATACATA
CAAGATCCTCCTGTCCGTTAGTGCATTCAATAACTGTCATTCTCATACATA
ATCAACCCATTGAAATTAAATACCAACATCAATGTGAAGCTGAACCTGGTTAATATAA
TACCTATTGTATAAGACCTTACTGATTCCATTATGTCGCATTGTTAAGATAAAACT
TCTTCATAGGAAAAAAAAAA



U. S. DEPARTMENT OF COMMERCE
PATENT AND TRADEMARK OFFICE

229/249

FIGURE 226

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77301
><subunit 1 of 1, 513 aa, 1 stop
><MW: 58266, pI: 9.84, NX(S/T): 4
MGFN VIRLLSGSAVALVIAPTVLLTMLSSAERGCPKGCRC EGMVYCESQKLQEIPSSISAG
CLGLSLRYNSLQKLKYNQFKGLNQLTWLYLDHNHISNIDENAFNGIRRLKELILSSNRISYF
LNNTFRPVTNLRNLDSYNQLHSLGSEQFRGLRKLLSLHLRSNSLRTIPVRIFQDCRNLELL
DLGYNRIRSLARNVFAGMIRLKELHLEHNQFSKLNLA FPRLVSLQONLYLQWNKISVIGQTM
SWTWSSLQRLLDLSGNEIEAFSGPSVFQCVNLQRLNLDNSNKLFIGQEILDWSWISLNDISLA
GNIWECSRNICSLVNWLKSFKGLRENTIICASPKELQGVNVIDAVKNYSICGKSTTERFDLA
RALPKPTFKPKLPRPKHESKPPLPTVGATEPGPETDADAEHISFHKIIAGSVALFLSVLVI
LLVIYVSWKRYPASMKQLQQRSLMRRHRKKRQSLKQMTPSTQE FYVDYKPTNTETSEMLLN
GTGPCTYNKSGSRECEV
```

Important features of the protein:

Signal peptide:

amino acids 1-33

Transmembrane domain:

amino acids 420-442

N-glycosylation sites.

amino acids 126-129, 357-360, 496-499, 504-507

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 465-468

Tyrosine kinase phosphorylation site.

amino acids 136-142

N-myristoylation sites.

amino acids 11-16, 33-38, 245-250, 332-337, 497-502, 507-512



230/249

FIGURE 227

AGTTCTGAGAAAGAAGGAATAAACACAGGCACCAACCCTATCCTAAGTTGACTGTCCTT
TAAATATGCAAGATCCAGACTTTCAGTGTACCTCAGCGATCTAACGATAGGGATCTG
TGTTGCCGCTATTCCAGTTGGTGCCTCGGACCTACCATGCGAAGAAGATGAAATGTGTG
AAATTATAATGACCAACACCCCTAATGGCTGGTATATCTGGATCCTCCTGCTGCTGGTTTGG
TGGCAGCTCTCTGTGGAGCTGTGGTCCCTGCCTCCAGTGCTGGCTGAGGAGACCCGA
ATTGATTCTCACAGGCGCACCATGGCAGTTTGCTGTTGGAGACTTGGACTCTATTATGG
GACAGAAGCAGCTGTGAGTCCAAC TGTTGGAATTACCTTCAAACCTCAAACCCCTGACCTAT
ATCCTGTTCCATGCTCCATGTTGCCCTTAGGCTCCCCACCTCCATATGAAGAAATTGTA
AAAACAACCTGATTTAGGTGTGGATTATCAATTAAAGTATTAACGACATCTGTAATTCCA
AAACATCAAATTAGGAATAGTTATTCAGTTGGAAATGTCCAGAGATCTATTATATA
GTCTGAGGAAGGACAATTGACAAAAGAATGGATGTTGGAAAAATTGGTCATGGAGATG
TTTAAATAGTAAAGTAGCAGGCTTGTGTCAGTGCTGTATCATACTTTATGCTACAC
AACCAAATTAAATGCTCTCCACTAGTATCCAAACAGGCAACAATTAGGTGCTGGAAGTAGTT
TCCATCACATTAGGACTCCACTGCAGTATACAGCACACCATTCTGCTTAAACTTTTC
CTAGCATGGGTCCATAAAATTATTATAATTAAACATAGCCCAGCCGAGAATCCAACAT
GTCCAGAACAGAACAGAAAGATAGTATTGAATGAAGGGTAAAGGATAAAATGAAGAGGAAAGGAAAGATTACAAGTCT
CAGCAAAACAAAGAGGTTATGCCAACCTGAAGAGGAAGAAATTGTAGATAGAAGGTGA
AGGAGATTGCTGAAGATATAGACATATAATGCCAACACGGGGAGAAAAGAAAATTCCC
CTTTACAGTAATGAATGTGGCCTCCATAGTCATAGTGTCTCTGGAGCCTCAGGGCTG
GCATTTATTGCAGCATCATGCTAACCTCGGCATAGGTATCTGTTCCATGAGGACTGC
AGAAGTAGCAATGAGACATCTCAAGTGGCATTGGCAGTGGCCATCAGCAGGGGGACAGA
CAAAACATCCATCACAGATGACATATGATCTCAGCTGACAAATTGTTGAACAAAACAAT
AAACATCAATAGATATCTAAAAA



231/249

FIGURE 228

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77303

><subunit 1 of 1, 146 aa, 1 stop

><MW: 16116, pI: 4.99, NX(S/T): 0

MSRSRLFSVTSAISTIGILCLPLFQLVLSDLPCEEDEMCVNNDQHPNGWYIWILLLVLA
ALLCGAVVLCLQCWLRRPRIDSHRRTMAVFAVGDLDSIYGTEAAVSPVGIIHLQTQTPDLYP
VPAPCFGPLGSPPPYEEIVKTT

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 52-70



232/249

FIGURE 229

GAGCGGAGTAAAATCTCCACAAGCTGGAACAAACCTCGTCCAACTCCCACCCACCGCGGT
 TTCTCCAGCTCGATCTGGAGGCTGCTCGCCAGTGTGGGACGCAGCTGACGCCGCTTATTA
 GCTCTCGCTCGCTGCCCGGCTCAGAAGCTCCGTGGCGGGCAGCGTACAGAGAACCCC
 ACGGCCAGCTCAGTTCTCTACTTTGGGAGAGAGAGAAAGTCAGATGCCCTTTAAACT
 CCCTCTCAAAACTCATCTCCTGGGTGACTGAGTTAATAGAGTGGATAACAACCTTGCTGAAG
 ATGAAGAATATACAATATTGAGGATATTTTTCTTTTTCAAGTCTTGATTTGTGGC
 TTACCTCAAGTTACCATTTTCAGTCAGTCTGTTGTTGCTTCTTCAGAA**ATGTTTTA**
 CAATCTCAAGAAAAAATATGTCAGAAATTGAGTTACTGTTGCTTGTATTTGGACTCATT
 TGGGGATTGATGTTACTGCACTATACTTTCAACAACCAAGACATCAAAGCAGTGTCAAGTT
 ACGTGAGCAAATACTAGACTTAAGAAAAGATATGTTAAAGCTCTAGCAGAGGAAAATAAGA
 ACACAGTGGATGTCGAGAACGGTCTATGGCAGGATATGCGGATCTGAAAAGAACAAATT
 GCTGTCCTCTGGATGACATTTGCAACGATTGGTGAAGCTGGAGAACAAAGTTGACTATAT
 TGTTGTGAATGGCTCAGCAGCCAACACCACCAATGGTACTAGTGGGAATTGGTGCCAGTAA
 CCACAAATAAAAGAACGAATGTCGGGCAGTATCAGA**TAG**CAGTTGAAAATCACCTGTGC
 TGCTCCATCCACTGTGGATTATATCCTATGGCAGAAAAGCTTATAATTGCTGGCTTAGGAC
 AGAGCAATACTTTACAATAAAAGCTCTACACATTTCAAGGAGTATGCTGGATTATGGAAC
 TCTAATTCTGTACATAAAATTAAAGTTATTGTTGCTTCAGGCAAGTCTGTTCAATG
 CTGTAATGTCCTTAAAGAGAATTGGTAATTGGTGTGATGTGGTAAGCAGATAGGTGAGT
 TTTGTATAAATCTTGTTGAGATCAAGCTGAAATGAAAACACTGAAAACATGGATTC
 ATTTCTATAACACATTATTAAGTATATAACACGTTTTGGACAAGTGAAGAATGTTAA
 TCATTCTGTCAATTGTTCTCAATAGATGTAACTGTTAGACTACGGCTATTGAAAAATGTG
 CTTATTGTAATATTGTTATTCCAATTATGAGCAGAGAAAAGGAAATATAATTGTTGAAAA
 TAATGTTTGAAATCATGACCCAAAGAACATGATTGACTATCCTCAGAATAACTGA
 AGGTTAATTATTGTATATTAAAGACTACCTTATAAGAGTATAATTGAAATGGGTAG
 CAGCCACTGTCCATTACCTATCGTAAACATGGGGCAATTAAATAACAGCATTAAAATAGTT
 GTAAAACCTAATCTTATACTTATTGAAGAATAAAAGATATTGATGAGAGTAACAATA
 AAGTATTGATTTTCACATACATGAATGTTCATTTAAAGTTAATTGCTTTATTATGGTC
 ATGCTATCAGGAAAGCACATTATTCATATTGGGTTATTGCTTTATTATGGTC
 TAGGAGGAAGGGACTTGGAGAATGGAACCTTGAGGACTTGTAGCCAGGTGTATATAATAAA
 GGTACTTTGTGCTGCATTAAATTGCTGGAAAGTGTAAACATTATATTATAAGAGTATC
 CTTTATGAAATTGTAATTGATATAACAGATGCATTAGATATTCAATTATATAATGGCAC
 TTAAAATAAGAACATTAAAATATAAACTATGAAGAGATTGACTATCTTTCAGGAAAAAGCT
 GTATATAGCACAGGGAACCTAATCTGGGTAAATTCTAGTATAAAACAAATTATAACTTTAT
 TTAATATTCCCTGTAGCAAATCTAATTGCCACATGGTGCCTATATTCAATTGTTATT
 CTCTATAGTAACTGCTTAAGTGCAGCTAGCTTAGACTATAGAATTGAAATTTATT
 TGTATTGTTCGTCATTATAATGCTACCACATGTAGCAATAATTACAATATTGTTATTAAAA
 TAAATATGTGAAATATTGTTCATGAAAGACAGATTCCAAATCTCTTCTCTCTGTA
 CTGTCTACCTTATGTGAAGAAATTAAATTATGCCATTGCCAGGT



233/249

FIGURE 230

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77648
><subunit 1 of 1, 140 aa, 1 stop
><MW: 15668, pI: 10.14, NX(S/T): 5
MFFTISRKNMSQKLSLLLLVFGЛИWGLMLLHYTFQQPRHQSSVKLREQILDLSKRYVKALAE
ENKNTVDVENGASMAGYADLKRTIAVLLDDILQRLVKLENKVDYIVVNGSAANTNGTSGNL
VPVTTNKRTNVSGSIR
```

Important features of the protein:

Signal peptide:

amino acids 1-26

**FIGURE 231**

CGCGGGCGGGCCGCCGGGTGAGCGTGCCGAGGC GGCTGTGGCGCAGGCTCCAGCCCCCAC
CATGCCGTGGCCCTGCTGCTGCTGGCCGTGAGTGGGGCCCAGACAAACCGGCCATGCT
TCCCCGGGTGCCAATGCGAGGTGGAGACCTCGGCCCTTCGACAGCTCAGCCTGACTCGG
GTGGATTGTAGCGGCCTGGGCCACATCATGCCGGTGCCTCCCTCTGGACACAGCCA
CTTGGACCTGTCCCTCAACCGGCTGGAGATGGTGAATGAGTCGGTGTGGCGGGCCGGCT
ACACGACGTTGGCTGGCCTGGATCTCAGCCACAACCTGCTCACCAGCATCTCACCCACTGCC
TTCTCCCGCTTCGCTACCTGGAGTCGCTGACCTCAGCCACAATGGCCTGACAGCCCTGCC
AGCCGAGAGCTTCACCAGCTACCCCTGAGCGACGTGAACCTAGCCACAACCAGCTCCGGG
AGGTCTCAGTGTCTGCCTCACGACGCACAGTCAGGGCCGGCACTACACGTGGACCTCTCC
CACAAACCTCATTCACCGCCTCGTGCCCAACCCACGAGGGCCGGCTGCCTGCGCCCACCAT
TCAGAGCCTGAACCTGGCCTGGAACCGGCTCCATGCCGTGCCAACCTCGAGACTTGGCCC
TGCCTACCTGAGCCTGGATGGGAACCCCTCTAGCTGTCTGGTCCGGTGCCTTCGCGGGG
CTGGGAGGCCTTACACACCTGTCTGGCCAGCCTGCAGAGGCTCCCTGAGCTGGCGCCAG
TGGCTTCGTGAGCTACCGGGCTGCAGGTCTGGACCTGTCGGGCAACCCCAAGCTTAAC
GGCAGGAGCTGAGGTGTTTCAGGCCTGAGCTCCCTGAGGAGCTGGACCTTCGGGCAACC
AACCTGGTGCCTGCCTGAGGCCTGCTCCTCACCTCCGGCACTGCAGAGCGTCAGCGT
GGGCCAGGATGTGGGTGCCGGCCTGGTGCAGGGCACCTACCCCGGAGGCCTGGCT
CCAGCCCCAAGGTGCCCTGCACTGCCTGAGACACCCGGGAATCTGCTGCCAGGGCCCCACC
ATCTTGTGACAAATGGTGTGGCCAGGGCACATAACAGACTGCTGTCCTGGGCTGCCTCAG
GTCCCGAGTAACTTATGTTCAATGTGCCAACACCAGTGGGGAGCCGCAGGCCTATGTGGCA
GCGTCACCACAGGAGTTGTGGGCCTAGGAGAGGCTTGGACCTGGAGGCCACACCTAGGAGC
AAAGTCTACCCCTTGTCTACGTTCTCCCAAACCATGAGCAGAGGGACTTCGATGCCA
AACCAAGACTCGGGTCCCTGCTTCCCTCCCCACTTATCCCCAAGTGCCTTCCTCAT
GCCTGGGCCGGCCTGACCCGCAATGGCAGAGGGTGGGACCCCTGCTGCAGGGCAGA
GTTCAGGTCCACTGGCTGAGTGTCCCCCTGGCCATGGCCCAGTCAGTCACTCAGGGCGAGTT
TCTTTCTAACATAGCCCTTCTTGCCATGAGGCCATGAGGCCCTCATCCTTTCTAT
TTCCCTAGAACCTTAATGGTAGAAGGAATTGCAAAGAATCAAGTCCACCCCTCATGTGAC
AGATGGGAAACTGAGGCCTTGAGAAGGAAAAGGCTAATCTAAGTTCTGCCAGTGGC
ATGACTGGGAGCACAGCCTCTGCCCTCCAGCCGGACCAATGCACTTTCTGCTCCTCTA
ATAAGCCCCACCCCTCCCCGCCTGGCTCCCTGCTGCCCTGCCCTGTTCCCCATTAGCACA
GGAGTAGCAGCAGCAGGACAGGCAAGAGCCTCACAAAGTGGGACTCTGGGCCTGACCAGCT
GTGGCGCATGGCTAACGTCACTCTGCCCTCGAGCCTCTGGAGCTAGGACAGCTAGGGCACATTGGTT
CCAGCCTAGCCAGTTCTACCCCTGGTTGGGTCCCCCAGCATCCAGACTGGAAACCTACC
CATTTTCCCTGAGCATCCTCTAGATGCTGCCCAAGGAGTTGCTGCAGTTCTGGAGCCTCA
TCTGGCTGGGATCTCAAGGGCCTCCTGGATTCAAGTCCCCACTGCCCTGAGCACGACAGC
CCTTCTTACCCCTCCAGGAATGCCGTGAAAGGAGACAAGGTCTGCCGACCCATGTCTATGC
TCTACCCCAAGGGCAGCAGCATTCTCAGCTCCGAACCTGGGCTGTTCCCTAGTCTTCA
TAAAAGTTGTTGCCCTTTAACGGAGTGTCACTTCAACCGGCCTCCCTACCCCTGCTGGC
CGGGGATGGAGACATGTCAATTGTAAGCAGAAAAAGGTTGCATTGTTCACTTTGTAAT
ATTGTCCTGGGCCTGTTGGGTGTTGGGGAGCTGGGCATCAGTGGCCACATGGGCATC
AGGGGCTGGCCCCACAGAGACCCACAGGGCAGTGAAGCTCTGCTTCCCCCACCTGCCCTAGC
CCATCATCTAACCCTGCTTGATTAAACACTATAAAAGGTTAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAA



SEARCHED SERIALIZED INDEXED FILED DECEMBER 17 2002

235/249

FIGURE 232

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77652
><subunit 1 of 1, 353 aa, 1 stop
><MW: 37847, pI: 6.80, NX(S/T): 2
MPWPLLLLLAVSGAQTTRPCFPGCQCEVETFGLFDSFSLDRVDCSGLGPHIMPVPIPLDTAH
LDLSSNRLEMVNESVLAGPGYTTLAGLDLSHNLLTSISPTAFSRLRYLESLDLSHNGLTALP
AESFTSSPLSDVNLSHNQLREVSVAFTTHSQGRALHVDLSHNLIHRLVPHPTRAGLPAPTI
QSLNLAWNRLHAVPNLRDPLRVLSDLGNPLAVIGPGAFAGLGGLTHLSLASLQRLPELAPS
GFRELPGLQVLDLSGNPKLNWAGAEVFSGLSSLQELDLSGTNLVPLPEALLLHLPALQSVSV
GQDVRCRRLVREGTYPRRPGSPPKVPLHCVDTRESAARGPTIL
```

Signal peptide:

amino acids 1-16

Transmembrane domains:

amino acids 215-232, 287-304



236/249

FIGURE 233

GATGGCGCAGCCACAGCTTCTGTGAGATTGATTCGATTCTCCCCAGTTCCCTGTGGGTCTGAGG
GGACCAGAAGGGTGAGCTACGTTGGCTTCTGGAAGGGGAGGCTATATGCGTCAATTCCCCA
AAACAAGTTTGACATTCCCCTGAAATGTCATTCTATCTATTCACTGCAAGTGCCTGCT
GTTCCAGGCCTTACCTGCTGGCACTAACGGCGGAGCCAGGATGGGACAGAATAAAGGAGC
CACGACCTGTGCCACCAACTCGCACTCAGACTCTGAACCTAGACCTGAAATCTCTTCA
GGGAGGCTTGGCAGTTTCTTACTCCTGTGGTCTCCAGATTCAAGGCCTAAGATGAAAGCC
TCTAGTCTGCCTTCAGCCTCTCTGCTGCGTTATCTCCTATGGACTCCTCCACTGG
ACTGAAGACACTCAATTGGAGCTGTGATGCCACAAACCTCAGGAAATACGAAATG
GATTTCTGAGATA CGGGGCAGTGTGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTA
AGGAGGACTGAGTCTTGCAAGACACAAAGCCTGCGAATCGATGCTGCCCTGCGCCATT
GCTAAGACTCTATCTGGACAGGGTATTTAAAAACTACCAGACCCCTGACCATTATACTCTCC
GGAAGATCAGCAGCCTGCCAATTCTTCTTACCATCAAGAAGGACCTCCGGCTCTCAT
GCCACATGACATGCCATTGTGGGAGGAAGCAATGAAGAAATACAGCCAGATTGAGTCA
CTTGAAAAGCTGGAACCTCAGGCAGCAGTTGTGAAGGCTTGGGGAACTAGACATTCTTC
TGCAATGGATGGAGGAGACAGAATAGGAGGAAAGTGTGCTGCTAAGAATATTGAGGT
CAAGAGCTCCAGTCTCAATACCTGCAAGAGGAGGCATGACCCAAACCACCATCTCTTACT
GTACTAGTCTTGTGCTGGTCACAGTGTATCTTATTGCAATTGCTTGTGCTTGCATGAT
TGTCTTATGCATCCCCAATCTTAATTGAGACCATACTTGTATAAGATTTGTAATATCTT
TCTGCTATTGGATATATTATTAGTTAATATATTATTATTGCTATTAAATGTATT
ATTTTTTACTTGGACATGAAACTTTAAAAAAATTCACAGATTATTTATAACCTGACTAG
AGCAGGTGATGTATTTTATACAGTAAAAAAAAACCTGTAAATTCTAGAAGAGTGGCT
AGGGGGGTATTCAATTGTATTCAACTAAGGACATATTACTCATGCTGATGCTCTGTGAGA
TATTGAAATTGAACCAATGACTACTTAGGATGGGTGTGGAATAAGTTGATGTGGAATT
GCACATCTACCTACAATTACTGACCATCCCCAGTAGACTCCCCAGTCCATAATTGTGTAT
CTTCCAGCCAGGAATCCTACACGGCCAGCATGTATTCTACAAATAAGTTCTTGCATA
CCAAAAAA



237/249

FIGURE 234

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA83500
><subunit 1 of 1, 261 aa, 1 stop
><MW: 29667, pI: 8.76, NX(S/T): 0
MRQFPKTSFDISPEMSFSIYSLQVPAVPGLTCWALTAEPGWGQNKGATTCATNSHSDSELRP
EIFSSREAWQFFLLLWSPDFRPKMKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNL
QEIRNGFSEIRGSVQAKDGNIDIRILRRTESLQDTK PANRCCLLRHLLRLYLDRVFKNYQTP
DHYTLRKISSLANSFLTICKDLRLSHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVKALG
ELDILLQWMEETE
```

Important features of the protein:

Signal peptide:

amino acids 1-42

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 192-195, 225-228

N-myristoylation sites.

amino acids 42-47, 46-51, 136-141



2 13 03 17 22 25 28 32 36 39 43 47 51 55 59 63 67 71 75 79

238/249

FIGURE 235

CCGTTATCGTCTTGCCTACTGCTGAATGTCCGTCCGGAGGAGGAGAGGCTTTGCCG
CTGACCCAGAGATGGCCCCGAGCGAGCAAATTCTACTGTCCGGCTGCCGGCTACCGTGGC
CGAGCTAGCAACCTTCCCCTGGATCTCACAAAAACTCGACTCCAAATGCAAGGAGAACAG
CTCTGCTCGGTTGGAGACGGTGCAAGAGAAATCTGCCCTATAGGGAAATGGTGCGCACA
GCCCTAGGGATCATTGAAGAGGAAGGCTTCTAAAGCTTGCAAGGAGTGACACCCGCCAT
TTACAGACACGTAGTGTATTCTGGAGGTCGAATGGTCACATATGAACATCTCCGAGAGGTTG
TGTTTGGCAAAAGTGAAGATGAGCATTATCCCCTTGGAAATCAGTCATTGGAGGGATGATG
GCTGGTGTATTGCCAGTTTAGCCAATCCAATGACCTAGTGAAGGTTCAGATGCAAAT
GGAAGGAAAAGGAAACTGGAAGGAAAACCATTGCGATTCGTGGTGTACATCATGCATTG
CAAAATCTAGCTGAAGGAGGAATACGAGGGCTTGGGCAGGCTGGTACCAATATAACAA
AGAGCAGCACTGGTGAATATGGGAGATTAAACCACTTATGATACAGTGAAACACTACTGGT
ATTGAATAACCACTTGAGGAACATATCATGACTCACGGTTATCAAGTTATGTTCTGGAC
TGGTAGCTTCTATTCTGGGAACACCAGCCGATGTCATCAAAGCAGAATAATGAATCAACCA
CGAGATAAACAGGAAGGGACTTTGTATAAATCATCGACTGACTGCTTGATTAGGCTGT
TCAAGGTGAAGGATTGAGTCTATATAAAGGCTTTACCATCTGGCTGAGAATGACCC
CTTGGTCAATGGTGTCTGGCTACTTATGAAAAAATCAGAGAGATGAGTGGAGTCAGTCCA
TTTTAA



U. S. PATENT AND TRADEMARK OFFICE

239/249

FIGURE 236

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77568
><subunit 1 of 1, 323 aa, 1 stop
><MW: 36064, pI: 9.33, NX(S/T): 1
MSVPEEEERLLPLTQRWPRASKFLLSGCAATVAELATFPLDLTKTRLQMQGEAALARLGDGA
RESAPYRGMVRTALGIIEEGFLKLWQGVTPAIYRHVVYSGGRMVTYEHLREVVFGKSEDEH
YPLWKSVIGGMMAGVIGQFLANPTDLVKVQMOMEGKRKLEGKPLRFRGVHHAFAKILAEGGI
RGLWAGWVPNIQRAALVNMGDLTTYDTVKHYLVLNTPLEDNIMTHGLSSLCGLVASILGTP
ADVIKSRIIMNQPRDKQGRGLLYKSSTDCLIQAVQGEGFMSLYKGFLPSWLRTMTPWSMVFWLT
YEKIREMSGVSPF
```

Transmembrane domains:

amino acids 25-38, 130-147, 233-248



20091223000000000000

240/249

FIGURE 237

CGGACGCGTGGCGCGGGACGCCGGCAGGGTTGTGGCGCAGCAGTCTCCTCCTGCAGCGC
GCCTGAAGTCGGCGTGGCGTTGAGGAAGCTGGGATACAGCATTAAATGAAAAATTTATGC
TTAAGAAGTAAAAATGGCAGGCTCCTAGATAATTTCGTTGCCAGAATGTGAATGTATTG
ACTGGAGTGAGAGAAGAAATGCTGTGGCATCTGTTGTCGCAGGTATATTGTTTTACAGGC
TGGTGGATAATGATTGATGCAGCTGTGGTGTATCCTAACGCCAGAACAGTTGAACCAGCCTT
TCACACATGTGGTGTATTTCCACATTGGCTTCTTCATGATAATGCTGTATCCAATGCTC
AGGTGAGAGGTGATAGCTATGAAAGCGGCTGTTAGGAAGAACAGGTGCTCGAGTTGGCTT
TTCATTGGTTCATGTTGATGTTGGTCACTTATTGCTTCATGTGGATTCTTTGGTGC
ATATGTTACCCAAAATACTGATGTTATCCGGGACTAGCTGTGTTTTCAAAATGCACCTTA
TATTTTAGCACTCTGATCTACAAATTGGAAGAACCGAAGAGCTATGGACTGAGATCAC
TTCTTAAGTCACATTTCTTTGTTATATTCTGTTGAGATAGGTTTTATCTCTCAGT
ACACATTGCCAAATGGAGTAGATTGTACATTAATGTTTGTTCATTCATTGACACTGTTAATATGTA
TGAGTTTGAAATAGTTTATGAAATTCTTATTTCTTATTGCAAGACTGTTAATATGTA
TATAATACAAGACTATATGAATTGGATAATGAGTATCAGTTTTATTCTGAGATTAGAA
CTTGATCTACTCCCTGAGCCAGGGTTACATCATCTGTCATTTAGAAGTAACCACTCTTGT
CTCTCTGGCTGGCACGGTGGCTATGCCTGTAATCCCAGCATTGGGAGGCCAGGG
CCGATTGCTTGAGGTCAAGTGTGAGACCAAGCCTGGCAACATGGCAAACCCCCATCTACT
AAAAATACAAAAATTAGCCAGGCATGGTGGTGGTGCCTGTAATCCCAGCTACCTGGGAGGC
TGAGGCAGGAGAATCGCTGAACCCGGGGCAGAGGTTGCAGTGAGCTGAGTTGCGCCAC
TGCACCTAGCCTGGGGAGAAAGTGAACACTCCCTCTAAAAAAAGACCACTCTCAGTATC
TCTGATTCTGAAGATGTACAAAAAAATAGCTTCATATCTGGAATGAGCACTGAGCCA
TAAAAGGTTTCAGCAAGTTGTAACCTATTGCTTAAATGAGGTTTTGGTAAAGA
AAAAATATTGTTCTTATGTATTGAAGAAGTGTACTTTATATAATGATTTTAAATGCC
AAAGGACTAGTTGAAAGCTTCTTTAAAAAGAATTCCCTCTAATATGACTTATGTGAGAA



2025 RELEASE UNDER E.O. 14176

241/249

FIGURE 238

MAGFLDNFRWPECECIDWSERRNAVAVSVVAGILFFTGWWIMIDAAVVYPKPEQLNHAFHTCG
VFSTLAFFMINAVSNAQVRGDSYESGCLGRTGARVWLFIGFMLMFGSLIASMWILFGAYVTQ
NTDVYPGLAVFFQNALLIFFSTLIYKFGRTEELWT

Important features:

Signal peptide:

amino acids 1-44

Transmembrane domains:

amino acids 23-42 (type II), 60-80, 97-117, 128-148



242/249

FIGURE 239

GTTGATGGCAAACCTCCTCAAAGGAGGGCAGAGCCTGCGCAGGCAGGAGCAGCTGGCCCA
CTGGCGGCCCGCAACACTCCGTCTCACCTCTGGGCCACTGCATCTAGAGGAGGGCCGTCT
GTGAGGCCACTACCCCTCCAGCAACTGGGAGGTGGACTGTCAGAAGCTGGCCAGGGTGGT
GGTCAGCTGGTCAGGGACCTACGGCACCTGCTGGACCACCTCGCCTCTCCATCGAACAG
GGAAGTGGAGGCCCTCGAGCCCTCGGTGGAAGCTGACCCAAAGCCACCCCTCACCTGGACAG
GATGAGAGTGTCAAGGTGTGCTTCGCCTCCTGGCCTCATCTTGCCATAGTCACGACATGGA
TGTTTATTGAAAGCTACATGAGCTTCAGCATGAAAACCATCCGTCTGCCACGCTGGCTGGCA
GCCTCGCCCACCAAGGAGATCCAGGTTAAAAAGTACAAGTGTGGCCTCATCAAGCCCTGCC
AGCCAACACTTTGCCTTAAAATCTGCAGTGGGCCAACGTCGTGGCCCTACTATGT
GCTTGAAAGACCGCATGATCATGAGTCCTGTGAAAAACAATGTGGCAGAGGCCTAACATC
GCCCTGGTGAATGGAACCACGGGAGCTGTGCTGGACAGAAGGCATTGACATGTACTCTGG
AGATGTTATGCACCTAGTGAAATTCTTAAAGAAATTCCGGGGGTGCACGTGGTGTGGTGG
CCTCCTACGACGATCCAGGGACAAAATGAACGATGAAAGCAGGAAACTCTCTGACTTG
GGGAGTT CCTACGAAAACA ACTGGCTTCCGGACAGCTGGTCTTCATAGGAGCAAAGA
CCTCAGGGTAAAAGCCC TTGAGCAGTTCTAAAGAACAGCCCAGACACAAACAAATACG
AGGGATGCCAGAGCTGGAGATGGAGGGCTGCATGCCCGAAGCCATT **TAG**GGTGGC
TGTGGCTCTCCTCAGCCAGGGCCTGAAGAACAGCTCCTGCCTGACTTAGGAGTCAGAGCCCG
GCAGGGGCTGAGGAGGAGGAGCAGGGGTGCTGCGTGGAAAGGTGCTGCAGGTCTGCACGC
TGTGTCGCGCCTCCTCGAACAGAACCCCTCCCACAGCACATCCTACCCGAAGACC
AGCCTCAGAGGGCTTCTGGAACCAGCTGTCTGGAGAGAAATGGGGTGCTTCGTCAAGGG
ACTGCTGACGGCTGGCCTGAGGAAGGACAAACTGCCAGACTTGAGCCCAATTAAATTAA
TTTTGCTGGTTTGAAAAAAAAAAAAAA



U.S. PATENT & TRADEMARK OFFICE

243/249

FIGURE 240

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59814
<subunit 1 of 1, 224 aa, 1 stop
<MW: 24963, pi: 9.64, NX(S/T): 1
MRVSGVLRLLALIFAIVTTWMFIRSYMSFSMKTIRLPRWLAASPTKEIQVKKYCGLIKPCP
ANYFAFKICSGAANVVGPTMCFEDRMIMSPVKNNVGRGLNIALVNNGTTGAVLGQKAFDMYSG
DVMHLVKFLKEIPGGALVLVASYDDPGTKMNDESRKLFSDLGSSYAKQLGFRDSWVFIGAKD
LRGKSPFEQFLKNSPDTNKYEGWPELLEMEGCMPKPF
```

Important features:

Signal peptide:

amino acids 1-15

ATP/GTP-binding site motif A (P-loop).

amino acids 184-191

N-glycosylation site.

amino acids 107-110



2025 RELEASE UNDER E.O. 14176

244/249

FIGURE 241

GAGACTGCAGAGGGAGATAAAGAGAGAGGGCAAAGAGGCAGCAAGAGAGTTGTCTGGGGAT
CCAGAAACCCATGATACCCTACTGAACACCGAATCCCCTGGAAGGCCACAGAGACAGAGACA
GCAAGAGAAGCAGAGATAAATACACTCACGCCAGGAGCTCGCTCGCTCTCTCTCTC
TCACTCCTCCCTCCCTCTCTGCCTGTCCTAGTCCTCTAGTCCTCAAATTCCCAGTCCC
CTGCACCCCTTCCTGGGACACTATGTTGTTCTCCGCCCTCGCTGGAGGTGATTGGATCC
TGGCTGCAGATGGGGGTCAACACTGGACGTATGAGGGCCCACATGGTCAGGACCATTGCCA
GCCTCTTACCCCTGAGTGTGGAAACAATGCCAGTCGCCATCGATATTGAGACAGACAGTGT
GACATTGACCTGATTCGCCTGCTCTGCAGCCCCACGGATATGACCAGCCTGGCACCGAGC
CTTGGACCTGCACAACAATGCCACACAGTGCAACTCTCTGCCCTCACCTGTATCTG
GGTGGACTTCCCCGAAAATATGTAGCTGCCAGCTCACCTGCACTGGGTGAGAAAGGATC
CCCAGGGGGTCAGAACACCAAGATCAACAGTGAAGCCACATTGCAGAGCTCCACATTGTAC
ATTATGACTCTGATTCCATGACAGCTTGAGTGAGGCTGCTGAGAGGCCCTCAGGGCTGGCT
GTCCTGGCATCCTAATTGAGGTGGTGAGACTAAGAATATAGCTTATGAACACATTCTGAG
TCACTTGATGAAGTCAGGCATAAAGATCAGAACACCTCAGTGCCCTCCCTAACCTAACAGAG
AGCTGCTCCCCAACAGCTGGGCAGTACTCCGCTACAATGGCTCGCTCACAACTCCCCCT
TGCTACCAGAGTGTGCTCTGGACAGTTTATAGAAGGTCCCAGATTCAATGGAACAGCT
GGAAAAGCTTCAGGGACATTGTTCTCCACAGAACAGAGGCCCTCTAACGCTCTGGTACAGA
ACTACCGAGCCCTTCAGCCTCTCAATCAGCGCATGGCTTGCTTCTTCATCCAAGCAGGA
TCCTCGTATACCACAGGTGAAATGCTGAGTCTAGGTGTAGGAATCTGGTGGCTGTCTG
CCTCTCCTGGCTTTATTCATTGCTAGAAAGATTGGAAGAACAGGGCTGGAAAACCGAA
AGAGTGTGGATGACTCCCTCATGCCATCAGGAAGCCTCTAAATGGGTGAGGATCTG
GCCAGAAACACTGTAGGAGTAGTAAGCAGATGCTCCTCCCTGGACATCTTAGAGAG
GAATGGACCCAGGCTGTCATTCCAGGAAGAACCTGAGAGCCTCAGCCTCTCCAAACATGTA
GGAGGAAATGAGGAAATCGCTGTGTTAATGCAGAGANCAAACCTGTTAGTTGCAGGG
GAAGTTGGATATACCCAAAGTCCTCTACCCCTCACTTTATGCCCTTCCAGATA
TACTGCGGGATCTCCTCTAGGATAAAGAGTTGCTGTTGAAGTTGATATTTGATCAATA
TATTGGAAATTAAAGTTCTGACTTT



245/249

FIGURE 242

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62812

><subunit 1 of 1, 337 aa, 1 stop

><MW: 37668, pI: 6.27, NX(S/T): 1

MLFSALLLEVIWILAADGGQHWTYEGPHGQDHWPASYP ECNNAQSPIDIQTDSVTFD PDL P
ALQPHGYDQPGTEPLDLHNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPGGSEHQ
INSEATFAELHIVHYDSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRH
KDQKTSVPPFNLRELLPKQLGQYFRYNGSLTPPCYQSVLWTVFYRRSQISMEQLEKLQGTL
FSTEEEPSKLLVQNYRALQPLNQRMVFASFIQAGSSYT GEMLSLGVGILVGCLCLLLAVYF
IARKIRKKRLENRKSVVFTSAQATTEA

Important features of the protein:

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 291-310

N-glycosylation site.

amino acids 213-216

Eukaryotic-type carbonic anhydrases proteins

amino acids 197-245, 104-140, 22-69



246/249

FIGURE 243



SEARCHED SERIALIZED INDEXED

247/249

FIGURE 244

MRSTILLFCLLGSTRSLPQLKPALGLPPTKLAPDQGTLPNQQQSNQVFPSSLIPLTQM
LTLPDPDLHLLNPAAGMTPGTQTHPLTLGGLNVQQQLHPHVLPIFVTQLGAQGTILSSEE
LPQIFTSLIIHSLFPGGILPTSQAGANPDVQDGSLPAGGAGVNPATQGT PAGRLPTPSG
TDDDFAVTPAGIQQRSTHAIEEATTESANGIQ

Signal peptide:

amino acids 1-16



248/249

FIGURE 245

GGAGAGAGGCGCGCGGGTGAAGGCGCATTGATGCAGCCTGCCGCGCCCTCGGAGCGCGGGCG
GAGCCAGACGCTGACCACGTTCTCCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCCTGCCCG
GCAGCCGGAGCC**ATG**CGACCCCCAGGGCCCCGCCGCCTCCCGCAGCAGGCTCCGCAGGCCCTCC
TGCTGCTCCTGCTGCTGCAGCTGCCGCGCCGTGAGCGCCTCTGAGATCCCCAAGGGGAAG
CAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGTGCTTACAAGG
GCCAGCAGGAGTGCCTGGTCAGACGGGAGCCCTGGGGCCAATGTTATTCCGGGTACACCTG
GGATCCCAGGTGGGATGGATTCAAAGGAGAAAAGGGGAATGTCTGAGGGAAAGCTTGAG
GAGTCCTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCAATTGAATTATGGCATAGATCT
TGGAAAATTGCGGAGTGTACATTACAAAGATGCAGAAATGCATGCTGTCAGCGTTGGTATTTCACATT
TCAGTGGCTCACTCGGCTAAATGCAGAAATGCATGCTGTCAGCGTTGGTATTTCACATT
AATGGAGCTGAATGTTAGGACCTCTCCCATTGAAGCTATAATTATTGGACCAAGGAAG
CCCTGAAATGAATTCAACAATTAAATTACATCGCACCTCTCTGTGGAAGGACTTGTGAAG
GAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGGTGGCACTGTTCAAGATTACCCAAAA
GGAGATGCTTCACTGGATGGAATTCAAGTTCTCGCATCATTATTGAAGAACTACCCAAAA**TA**
AATGCTTAATTCATTGCTACCTCTTTTATTATGCCTGGAATGGTTCACTAAAT
GACATTAAATAAGTTATGTATACATCTGAATGAAAAGCAAAGCTAAATATGTTACAGA
CCAAAGTGTGATTTCACACTGTTAAATCTAGCATTATTCAATTGCTCAATCAAAGT
GGTTCAATATTTTTAGTTGGTTAGAATACTTCTCATAGTCACATTCTCTCAACCTA
TAATTGGAATATTGTTGGTCTTTGTTCTTAGTATAGCATTAAAAAAATA
AAAAAGCTACCAATCTTGTACAATTGTAAGAATTTTTATATCTGTTAAAT
AAAAATTATTCCAACA

249/249

FIGURE 246

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393
><subunit 1 of 1, 243 aa, 1 stop
><MW: 26266, pI: 8.43, NX(S/T): 1
MRPQGPAAASPQRRLRGLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPAGV
PGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIA
ECTFTKMRNSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECGPLPIEAIYLDQGSPEMN
STINIHRRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIEELPK

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 195-217

